

FIGURE 1

08736019-102296



COUNTS 1-125

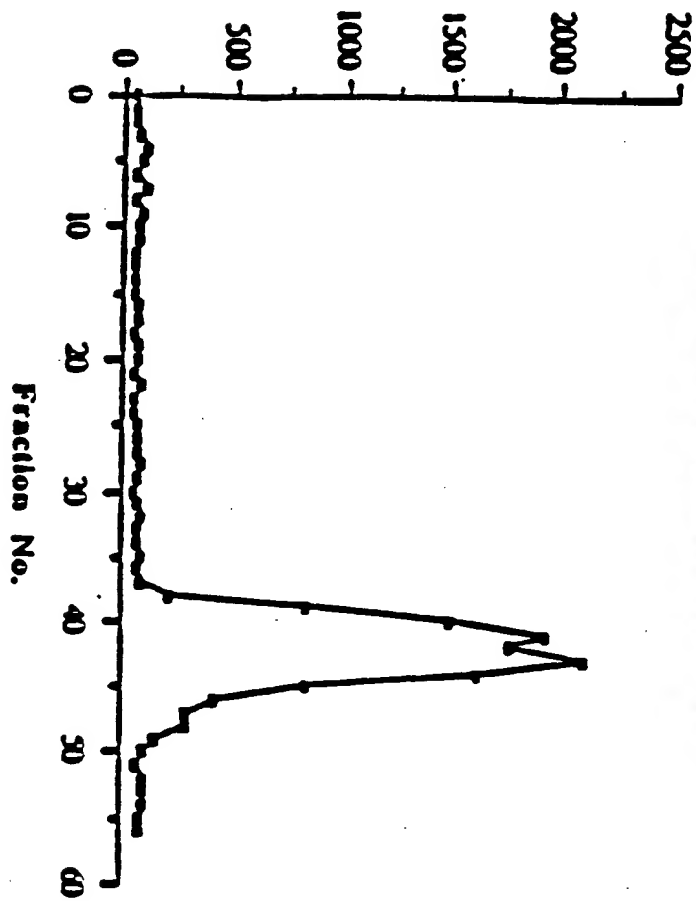


FIGURE 2

08736019-102296

Counts 1-125

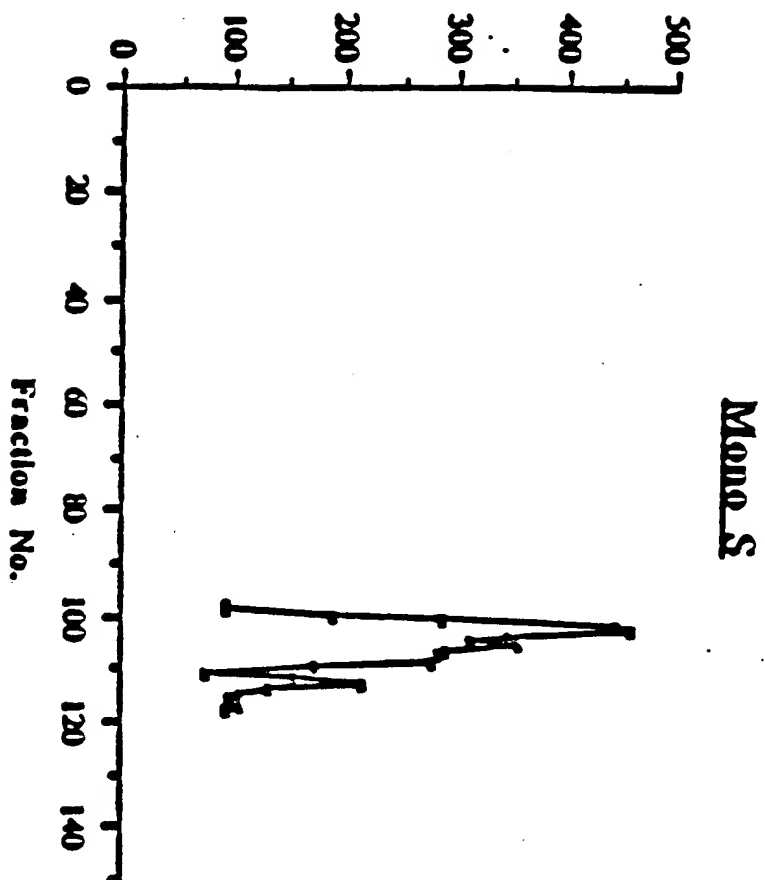
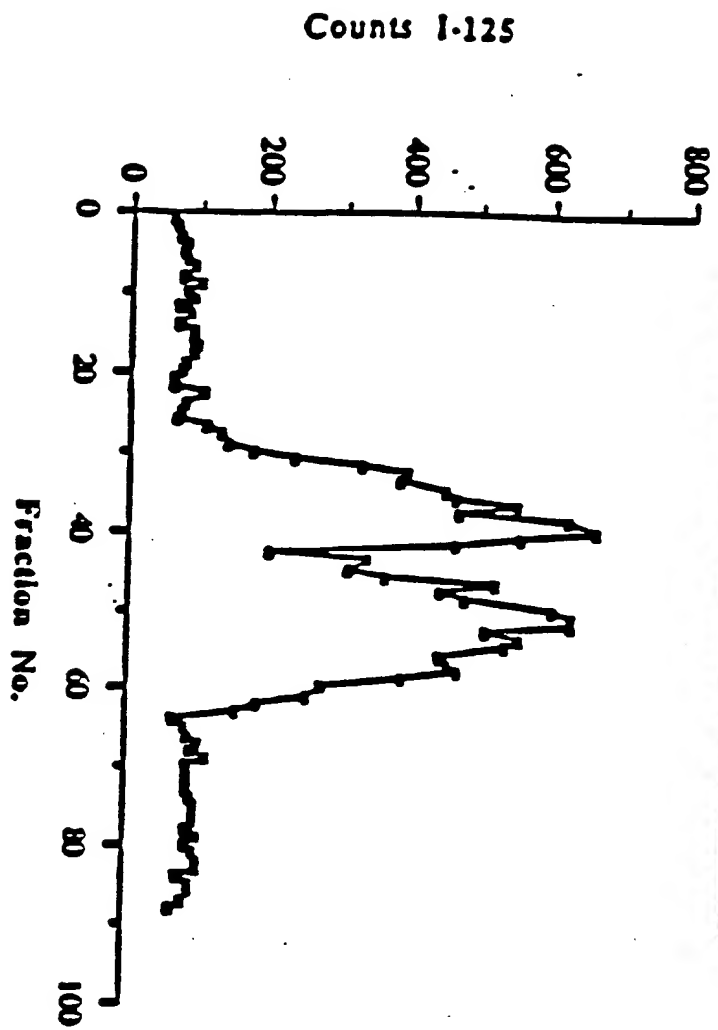


FIGURE 3

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**Superose 12 gel filtration FPLC**



**FIGURE 4**

08736019.102296

# Reversed phase HPLC

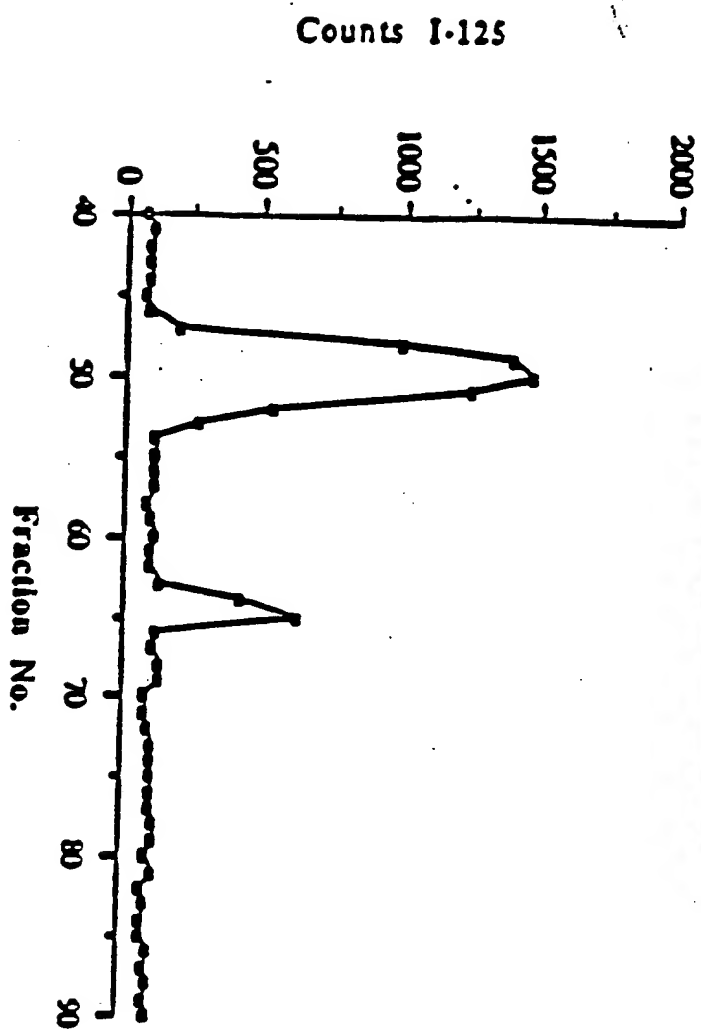


FIGURE 5

00736019-102296

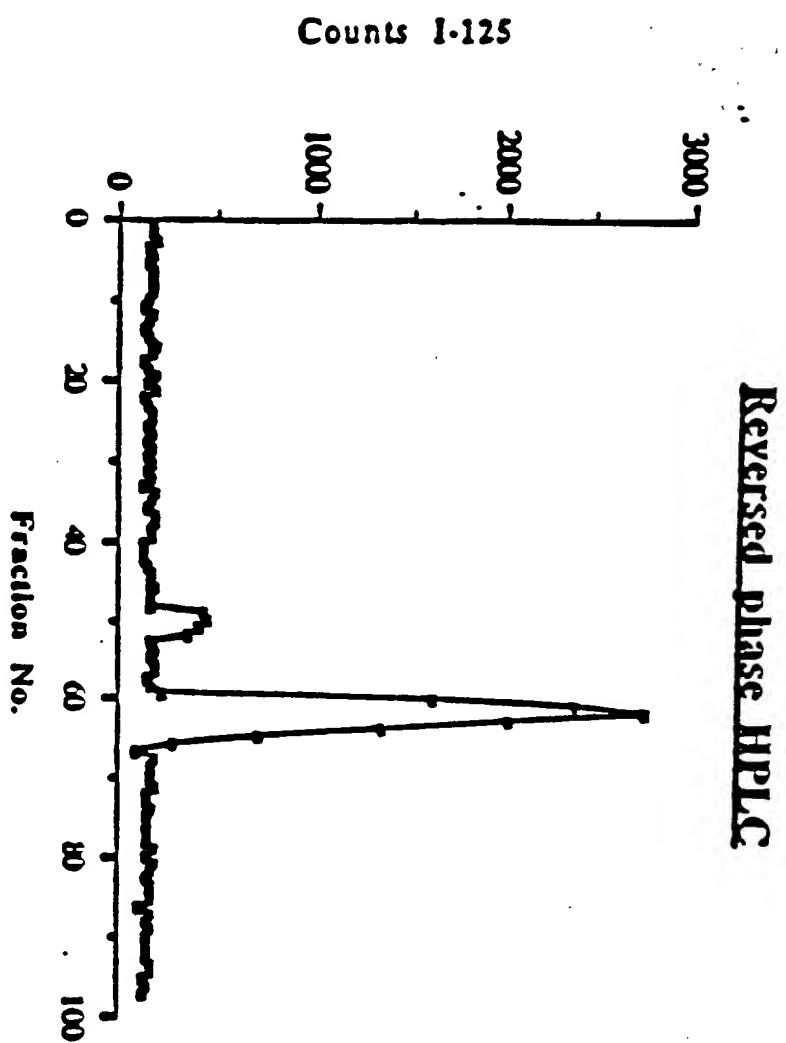


FIGURE 6

002736019-102296

Counts 1-125

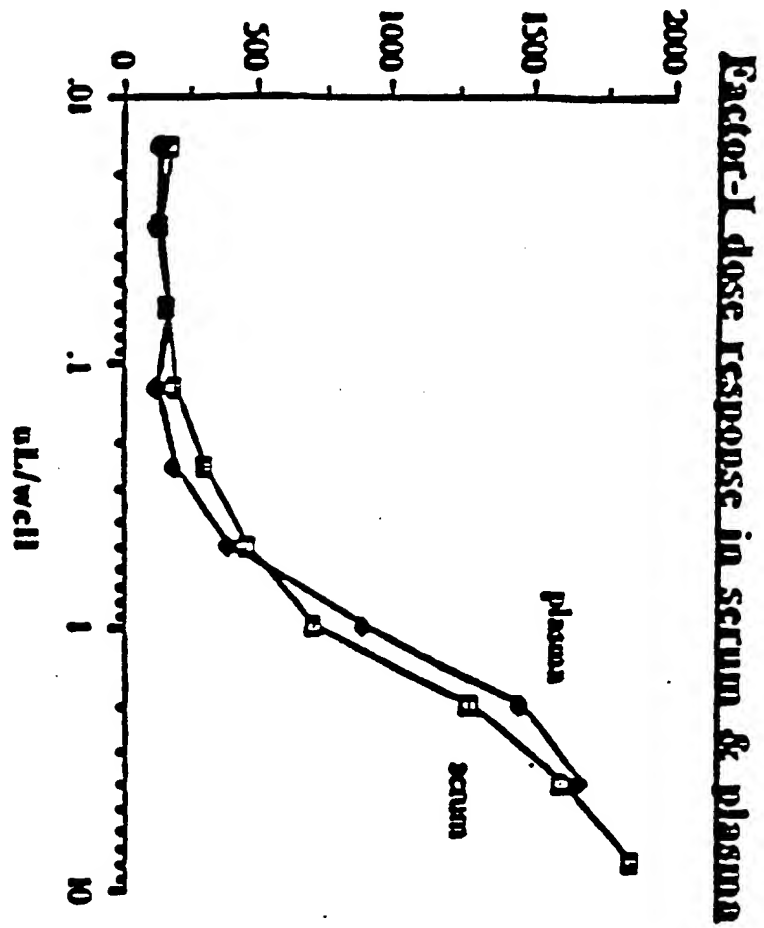


FIGURE 7

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Counts 1-125

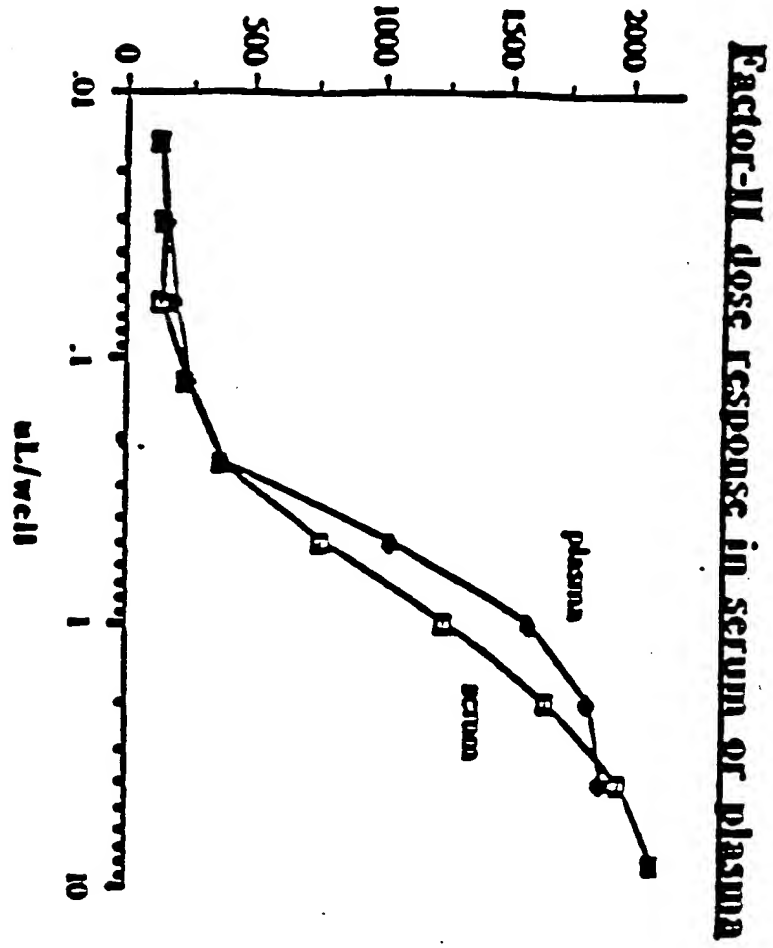


FIGURE 8

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FIGURE 9

IF-1 01

Normidine  
F K G D A H T E (seq ID no: 1)

IF-1 02

Tryptophan  
K M A S L A D E Y E Y M X K . (seq ID no: 2)

IF-1 03

K M T E T S S G L X L K . (seq ID no: 3)

IF-1 04

K M K L G E M W A E (seq ID no: 4)

IF-1 05

K M L G E K N A (seq ID no: 5)

IF-1 06

K M I K S E H A G L S I G D T A K . (seq ID no: 6)

IF-1 07

K M A S L A D E Y E Y M N K . (seq ID no: 7)

IF-1 08

K M I K G E H P G L S I G D V A K . (seq ID no: 8)

IF-1 09

K M S E Y A F F V O T X R . (seq ID no: 9)

IF-1 10

K M S E H P G L S I G D T A K . (seq ID no: 10)

IF-1 11

K M A G Y F A E X A R . (seq ID no: 11)

IF-1 12

K M K L E F L X A K . (seq ID no: 12)

IF-1 13

K M T T E M A S E O G A (seq ID no: 13)

IF-1 14

K M A K E A L A A L K . (seq ID no: 14)

IF-1 15

K M F V L O A K K . (seq ID no: 15)

IF-1 16

K M L G E M W (seq ID no: 16)

PMG-1

PMG-1

PMG-17

PMG-2

PMG-1

PMG-2

PMG-1

Protease V8 peptides

E T O P D P G O I L K K V P M V I G A Y T (seq ID no: 169)

E Y K C L K F K W F K K A T V M (seq ID no: 17)

E A K Y F S K X D A (seq ID no: 18)

E X K F Y V P (seq ID no: 19)

E L S F A S V R L P G C P P G V D P M V S F P V A L

Ubbold (seq ID no: 20)

Ubbold

IF-1 17

IF-1 18

IF-1 19

IF-1 20

IF-1 21

Figure 10

A

|          |   |                 |
|----------|---|-----------------|
| OCF-1 01 | F K G D A H T E                           | (Seq ID no: 1)  |
| OCF-1 02 | A S L A D E Y E Y M X K                   | (Seq ID no: 22) |
| OCF-1 03 | T E T S S S G L X L K                     | (Seq ID no: 23) |
| OCF-1 07 | A S L A D E Y E Y M X K                   | (Seq ID no: 24) |
| OCF-1 11 | A G Y F A E X A N                         | (Seq ID no: 25) |
| OCF-1 13 | T T E M A S E O G A                       | (Seq ID no: 26) |
| OCF-1 14 | A K E A L A A L K                         | (Seq ID no: 27) |
| OCF-1 15 | F V L O A K K                             | (Seq ID no: 28) |
| OCF-1 17 | E T O P D P G Q I L K K V P M V I G A Y T | (Seq ID no: 29) |
| OCF-1 18 | E Y K C L K F K M F K K A T V M           | (Seq ID no: 17) |

B

|          |                 |                 |
|----------|-----------------|-----------------|
| OCF-1 20 | E X K F Y V P   | (Seq ID no: 19) |
| OCF-1 12 | K L E F L X A K | (Seq ID no: 32) |

Figure 11

GGF-II 01 K/R VHQVWAAK\*  
GGF-II 02 K/R YIFFMEPEAXSSG  
GGF-II 03 K/R LGAWGPPAFPVX.Y  
GGF-II 04 K/R WVVVIEGK\*  
GGF-II 05 K/R ALAAAGYDVEK\*  
GGF-II 06 K/R LVLR\*  
GGF-II 07 K/R XXYPGQITSN  
GGF-II 08 K/R ASPVSVGSGVQELVQR\*  
GGF-II 09 K/R VCLLTVAALPPT  
GGF-II 10 K/R DLLLXV

Trypsin peptides

(SEQ ID NO: 45)  
(SEQ ID NO: 46)  
(SEQ ID NO: 47)  
(SEQ ID NO: 48)  
Histone H1 (SEQ ID NO: 164)  
(SEQ ID NO: 165)  
Trypsin (SEQ ID NO: 166)  
(SEQ ID NO: 49)  
(SEQ ID NO: 50)  
(SEQ ID NO: 53)

GF-II 11  
GF-II 12

Lysyl Endopeptidase-C peptides

KVHQVWAAK\*  
KASLADSGEYMXK\*

(SEQ ID NO: 51)  
(SEQ ID NO: 52)

Figure 12

A

|           |                 |                 |
|-----------|-----------------|-----------------|
| GGF-II 01 | VHQVWAAK        | (SEQ ID NO: 45) |
| GGF-II 02 | YIFFMEPEAXSSG   | (SEQ ID NO: 46) |
| GGF-II 03 | LGAWGPPAFPVXY   | (SEQ ID NO: 47) |
| GGF-II 04 | WFVVIEGK        | (SEQ ID NO: 48) |
| GGF-II 08 | ASPVSVGSVQELVQR | (SEQ ID NO: 49) |
| GGF-II 09 | VCLLTVAALPPT    | (SEQ ID NO: 50) |
| GGF-II 11 | KVHQVWAAK       | (SEQ ID NO: 51) |
| GGF-II 12 | KASLADSGEYMXK   | (SEQ ID NO: 52) |

B

Novel Factor II Peptides - others

|           |        |                 |
|-----------|--------|-----------------|
| GGF-II 10 | DLLLXV | (SEQ ID NO: 53) |
|-----------|--------|-----------------|

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# Comparison of BrUdR JSA and [ $^{125}$ I]UdR counting method for the DNA synthesis assay in Schwann cell cultures

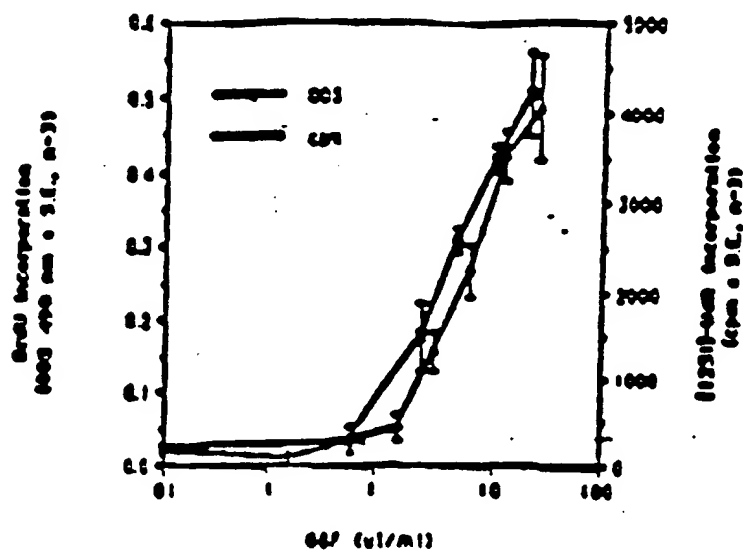


Fig. 13

## Comparison of Br-UdR immunoreactivity and Br-UdR labelled cell number

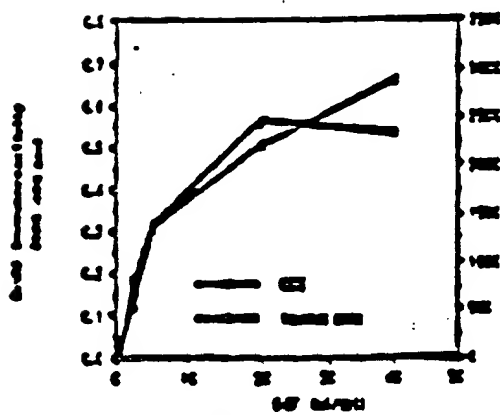


Fig. 14a

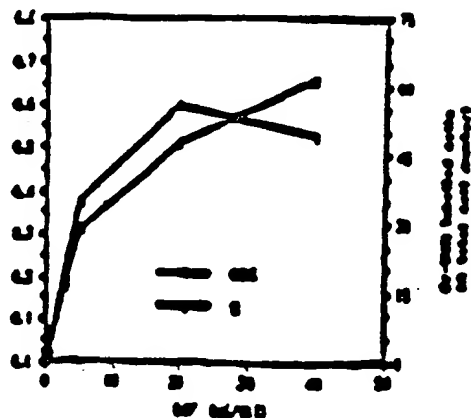


Fig. 14b.

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# Mitogenic response of rat sciatic nerve Schwann cell to GGFs

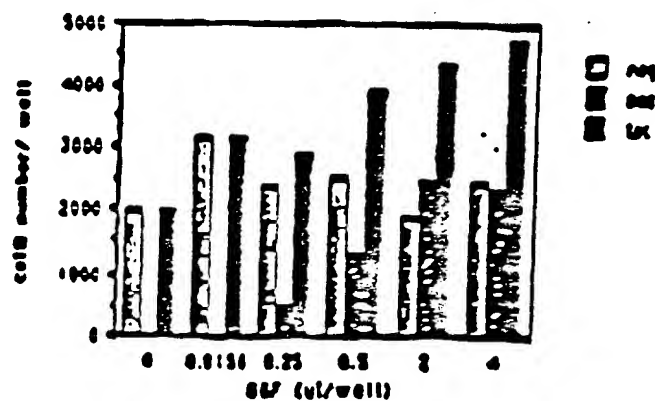


Fig 15

## DNA synthesis in rat sciatic nerve Schwann cells and 3T3 fibroblasts in the presence of GGFs

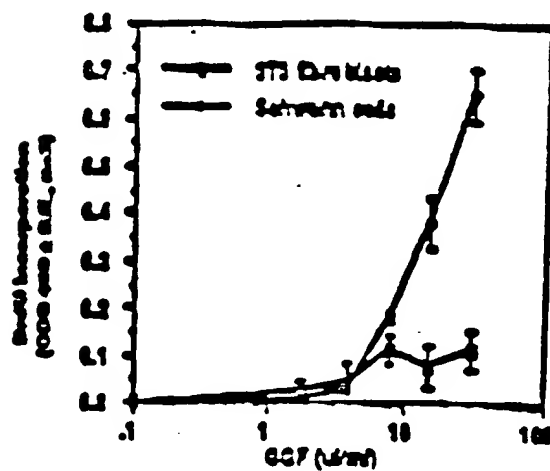


Fig 16.

# Mitogenic response of BHK 21 C13 cells to FCS and GGFs

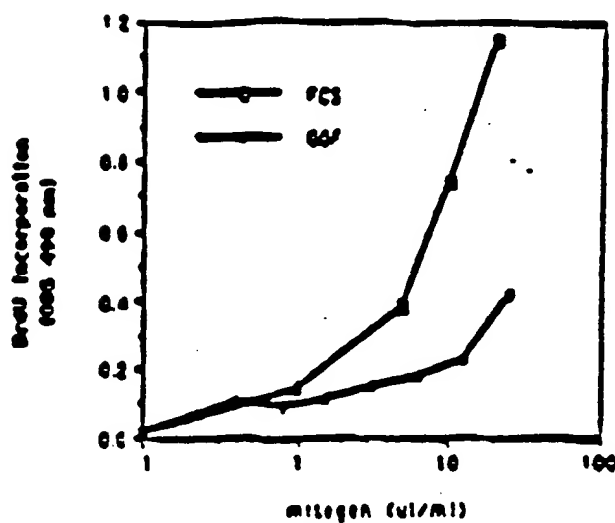


Fig. 17

## Survival and proliferation of BHK21 C13 cell microcultures after 48 hours in presence of GGFs

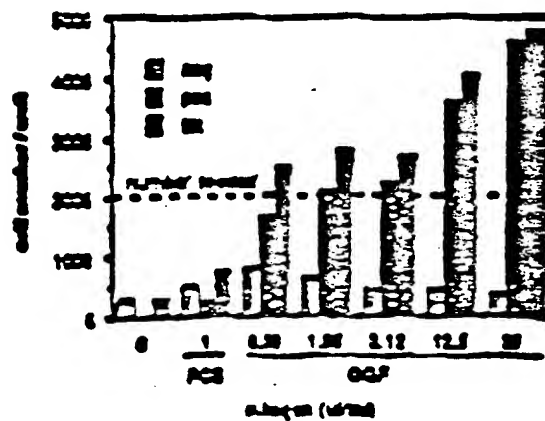


Fig. 18.

# Mitogenic response of C6 cells to FCS

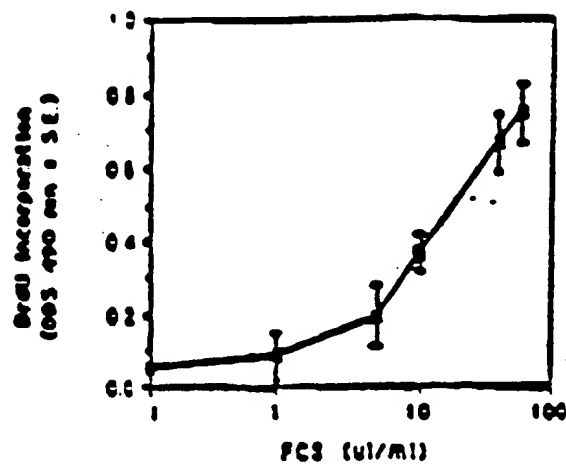


Fig 19.

# Mitogenic response of C6 cells to aFGF and GGFs

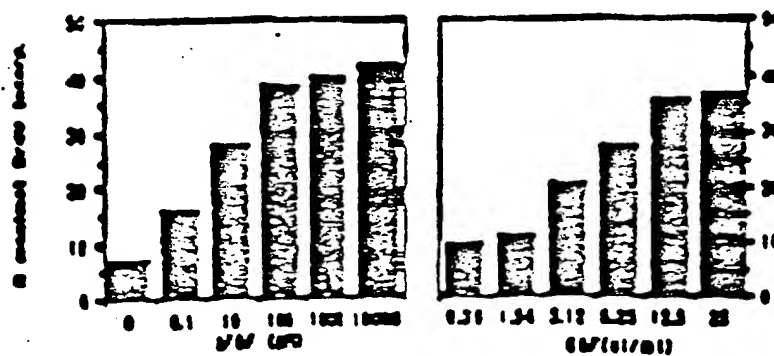


Fig 20

08736019-102296



FIGURE 21

## DECENTRATE OLIGONUCLEOTIDE PROBES FOR FACTOR I AND FACTOR II

| Oligo | Sequence                | Peptide  |                 |
|-------|-------------------------|----------|-----------------|
| 535   | TTTAAAGCGGAGYGCNCAYAC!  | GGFI-1   | (SER ID NO: 54) |
| 536   | CATRTAYTCTRTAYTCTRTGCG! | GGFI-2   | (SER ID NO: 55) |
| 537   | TGYYTCHGANGCCATYTCNGT!  | GGFI-13  | (SER ID NO: 56) |
| 538   | TGYYTCHGANGCCATYTCNGT!  | GGFI-13  | (SER ID NO: 57) |
| 539   | CCDATHACCATGCGXAGYTT!   | GGFI-17  | (SER ID NO: 58) |
| 540   | GCGGCCCAUACYTCTGAC!     | GGFII-1  | (SER ID NO: 59) |
| 541   | GCTTCNGGCTTCCATRAA!     | GGFII-2  | (SER ID NO: 60) |
| 542   | GCTTCGATACGACAAACG!     | GGFII-4  | (SER ID NO: 61) |
| 543   | TGCGCAUATACGCG!         | GGFI-12  | (SER ID NO: 62) |
| 544   | GCGCGXAGGCGTCTGTCG!     | GGFI-14  | (SER ID NO: 63) |
| 545   | GCGCGTAAAGCGTCTGTCG!    | GGFI-14  | (SER ID NO: 64) |
| 546   | TTTTCGCGTCTGACGAA!      | GGFI-15  | (SER ID NO: 65) |
| 551   | TTTTCGCGTCTGACGAA!      | GGFI-15  | (SER ID NO: 66) |
| 568   | TGACGACGCTCTGAC!        | GGFII-8  | (SER ID NO: 67) |
| 569   | TGACGACGCTCTGAC!        | GGFII-8  | (SER ID NO: 68) |
| 609   | CATRTAYTCHGCGARTCHGCG!  | GGFII-12 | (SER ID NO: 69) |
| 610   | CATRTAYTCHGCGARTCHGCG!  | GGFII-12 | (SER ID NO: 70) |
| 649   | NGARTCHGCGTAAAGGCGTT!   | GGFII-12 | (SER ID NO: 71) |
| 650   | NGARTCHGCGTAAAGGCGTT!   | GGFII-12 | (SER ID NO: 72) |
| 651   | RGTRTCHGCGTAAAGGCGTT!   | GGFII-12 | (SER ID NO: 73) |
| 652   | RGTRTCHGCGTAAAGGCGTT!   | GGFII-12 | (SER ID NO: 74) |
| 653   | NGARTCHGCGTAAAGGCGTT!   | GGFII-12 | (SER ID NO: 75) |
| 654   | NGARTCHGCGTAAAGGCGTT!   | GGFII-12 | (SER ID NO: 76) |
| 655   | RGTRTCHGCGTAAAGGCGTT!   | GGFII-12 | (SER ID NO: 78) |
| 656   | RGTRTCHGCGTAAAGGCGTT!   | GGFII-12 | (SER ID NO: 79) |
| 659   | ACGACGAGATGGCTGCG!      | GGFI-13  | (SER ID NO: 80) |
| 660   | ACGACGAGATGGCTGCG!      | GGFI-13  | (SER ID NO: 81) |
| 661   | CAYCARTGTTGGCGCGAA!     | GGFII-1  | (SER ID NO: 82) |
| 662   | TTYGTHGTHATEGACGAA!     | GGFII-4  | (SER ID NO: 83) |
| 663   | AARGCGAGYGCNCAYACG!     | GGFI-1   | (SER ID NO: 84) |
| 664   | GARGCGYTHGCGCGTTGAA!    | GGFI-14  | (SER ID NO: 85) |
| 665   | GTHGCGTCTGTHGCGGTT!     | GGFII-8  | (SER ID NO: 86) |
| 666   | GTHGCGTCTGTHGCGGTT!     | GGFII-8  | (SER ID NO: 87) |
| 694   | NACGTTTTCGAGGCTGCG!     | GGFI-17  | (SER ID NO: 88) |

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**069708**

**FIGURE 22**

# PCR PRIMERS FOR FACTOR I AND FACTOR II

FIGURE 23

## Degenerate PCR primers

| Oligo | Sequence                                | Peptide  |                  |
|-------|---|----------|------------------|
| 657   | CCGAAATTCCTGCAGGARAHCAGCENGAYCENGGI     | GGPII-17 | (SEQ ID NO: 90)  |
| 658   | AAGGATCCTGCAGHGTTRTANGCHCHATHACCATNGG!  | GGPII-17 | (SEQ ID NO: 91)  |
| 667   | CCGAAATTCCTGCAGGCHGAYTCHGCHGARTAYATGI   | GGPII-12 | (SEQ ID NO: 92)  |
| 668   | CCGAAATTCCTGCAGGCHGAYATYCHGCHGARTAYATI  | GGPII-12 | (SEQ ID NO: 93)  |
| 669   | AAGGATCCTGCAGHCHCATRTAYTCHCHGARTCI      | GGPII-12 | (SEQ ID NO: 94)  |
| 670   | AAGGATCCTGCAGHCHCATRTAYTCHCHGARTCI      | GGPII-12 | (SEQ ID NO: 95)  |
| 671   | CCGAAATTCCTGCAGAYCAAGTHTGGCHGCHAA!      | GGPII-1  | (SEQ ID NO: 96)  |
| 672   | CCGAAATTCCTGCAGATHTTYYTATGAGRCENGARG!   | GGPII-2  | (SEQ ID NO: 97)  |
| 673   | CCGAAATTCCTGCAGGGGGCHGCHGCHHTTYCHGT!    | GGPII-3  | (SEQ ID NO: 98)  |
| 674   | CCGAAATTCCTGCAGTGGTTYGTHTNATHGARGG!     | GGPII-4  | (SEQ ID NO: 99)  |
| 677   | AAGGATCCTGCAGGYTTHGCHGCHGCHGAYTGTGT!    | GGPII-1  | (SEQ ID NO: 100) |
| 678   | AAGGATCCTGCAGGCHYTCHGCHGCHGCHGCHAA!     | GGPII-2  | (SEQ ID NO: 101) |
| 679   | AAGGATCCTGCAGACHGCHGCHGCHGCHGCHGCHG!    | GGPII-3  | (SEQ ID NO: 102) |
| 680   | AAGGATCCTGCAGGYTTHGCHYTCHGCHGCHGCHGCHG! | GGPII-4  | (SEQ ID NO: 103) |
| 681   | CATRTAYTCHGCHGCHGCHGCHGCHGCHGCHGCHG!    | GGPII-2  | (SEQ ID NO: 104) |
| 682   | CCGAAATTCCTGCAGAAAGGCHGCHGCHGCHGCHG!    | GGPII-1  | (SEQ ID NO: 105) |
| 683   | GCHGCHGCHGCHGCHGCHGCHGCHGCHGCHGCHG!     | GGPII-14 | (SEQ ID NO: 106) |
| 684   | GCHGCHGCHGCHGCHGCHGCHGCHGCHGCHGCHG!     | GGPII-14 | (SEQ ID NO: 107) |
| 685   | TCHGCHGCHGCHGCHGCHGCHGCHGCHGCHGCHG!     | GGPII-1  | (SEQ ID NO: 108) |

## Unique PCR primers for Factor II

| Oligo | Sequence                                 | Comment           |                  |
|-------|--|-------------------|------------------|
| 711   | CATCGATCTGCAGGCTGATTCTCGAGAAATATATGTGCA! | 3' RACE           | (SEQ ID NO: 109) |
| 712   | AAGGATCCTGCAGGCHCATCTCGAGTGCAGATCGATT!   | 3' RACE           | (SEQ ID NO: 110) |
| 713   | CCGAAATTCCTGCAGTGCATGCAAGCTAGGAAATGCA!   | 3' RACE           | (SEQ ID NO: 111) |
| 721   | CATCGATCTGCAGGCTGATTCTCGAGAAATATATGTGCA! | 5' RACE           | (SEQ ID NO: 112) |
| 722   | AAGGATCCTGCAGGCHCATCTCGAGTGCAGATCGATT!   | 5' RACE; ANCHORED | (SEQ ID NO: 113) |
| 723   | AAGGATCCTGCAGGCHCATCTCGAGTGCAGATCGATT!   | EXON A            | (SEQ ID NO: 114) |
| 726   | CCGAAATTCCTGCAGGCHCATCTCGAGTGCAGATCGATT! | EXON A            | (SEQ ID NO: 115) |
| 771   | CATCGATCTGCAGGCTGATTCTCGAGAAATATATGTGCA! | EXONS 3-4         | (SEQ ID NO: 116) |
| 772   | ATACCGGCTGCAGGCHCATCTCGAGTGCAGATCGATT!   | (SEQ ID NO: 117)  | (SEQ ID NO: 117) |
| 773   | AAGGATCCTGCAGGCHCATCTCGAGTGCAGATCGATT!   | ANCHORED          | (SEQ ID NO: 118) |
| 776   | ATACCGGCTGCAGGCHCATCTCGAGTGCAGATCGATT!   | EXONS 3-4         | (SEQ ID NO: 119) |

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Summary of contiguous GGF-II cDNA structures and sequences

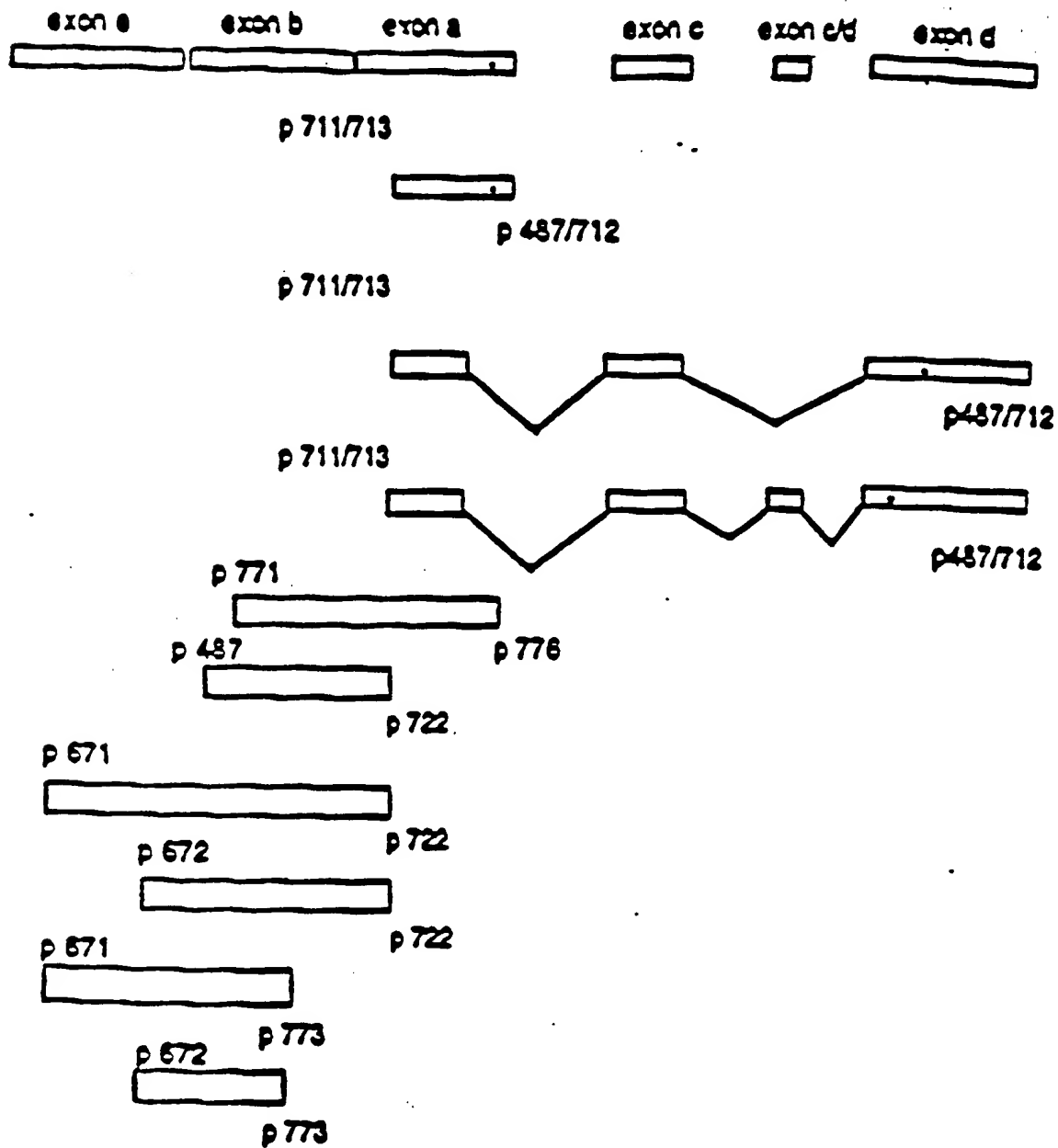
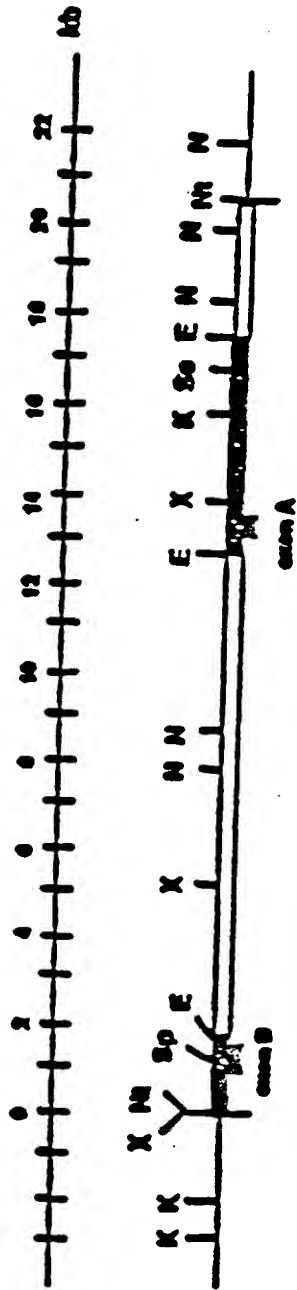


FIGURE 24

962220T 6T09E480

FIGURE 25



# Alternative gene products of putative bovine GGF-2



FIGURE 26

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OCF-II protein identified in deduced  
of putative bovine OCF-II proteins

16 sequences

| Peptide | Pos. | Sequence Match                                 |                                      |
|---------|------|--|--------------------------------------|
| II-1    | 1:   | VHGVAAK<br>HGVAAK AAGLR                        | (SEQ ID NO: 120)                     |
| II-10   | 14:  | DLLLV<br>GGLLV dellv RLGM.                     | (SEQ ID NO: 121)                     |
| II-03   | 21:  | LGAHGPPAFVXY<br>LLTVR lgaughpafpccg RLVD       | (SEQ ID NO: 122)<br>(SEQ ID NO: 123) |
| II-02   | 41:  | YIFTHPELVSSG<br>KEDSR YIFTHPELVSSG GPTL        | (SEQ ID NO: 124)<br>(SEQ ID NO: 125) |
| II-6    | 103: | LVL<br>VAGSK LVL CETSS                         | (SEQ ID NO: 126)                     |
| I-18    | 112: | EYKCLKFKWTKATVH<br>CETSS eyslklfkvfkngsal SRDK | (SEQ ID NO: 127)<br>(SEQ ID NO: 128) |
| II-12   | 151: | KSLADSGEYHCK<br>ELRIS KSLADSGEYHCK VISKL       | (SEQ ID NO: 129)<br>(SEQ ID NO: 130) |
| I-07    | 152: | ASLADIEYHCK<br>LRISK asladsgeyhck VISKL        | (SEQ ID NO: 131)<br>(SEQ ID NO: 132) |

FIGURE 27

08736019-102296

[illegible]



CONFIDENTIAL 100  
4 9 9 8  
CONFIDENTIAL 200

(SEQ ID NO: 134)

**FILE 288**

053619-101000



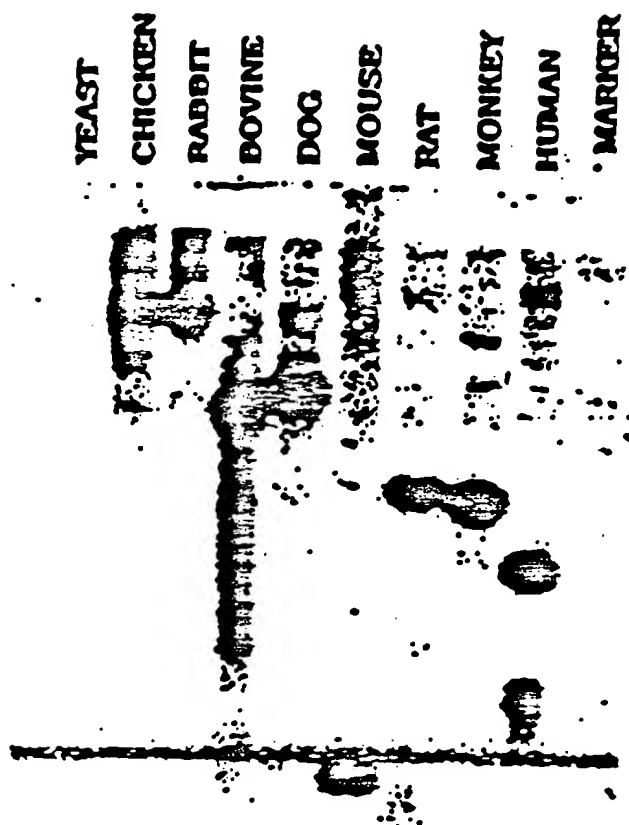
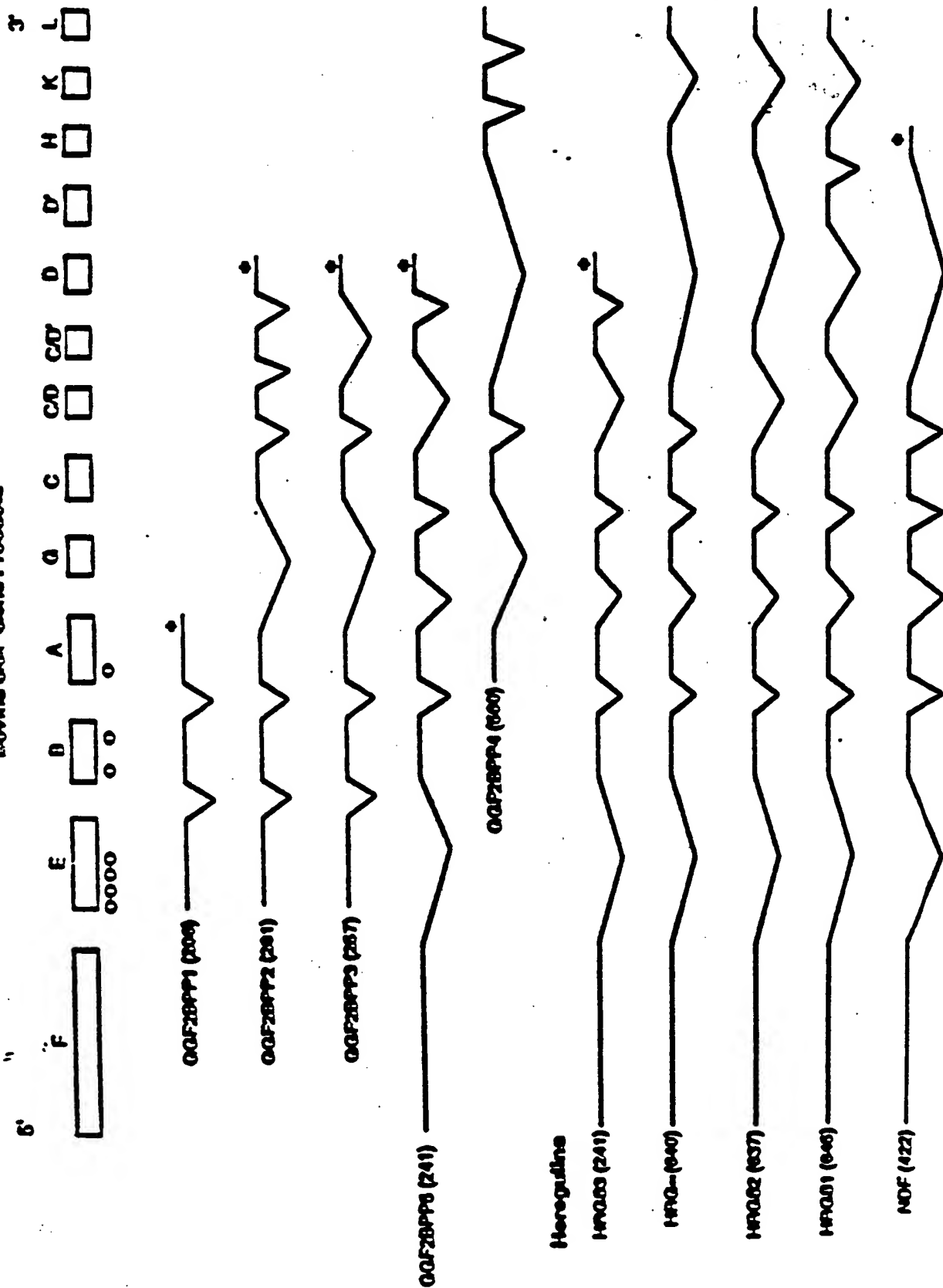


FIGURE 29

FIGURE 10

Revised GOF Gene Products



**CODING SIGNATURE P: (SEQ ID NO: 136)**

**CODING SHEET 2: (SEQ ID NO: 137)**

CCCATCAGTGTGCGGCGGCGAAGCGCGCGCTTGAAAGAGCACTCGCTGCTCAGCGTGC 60  
 H Q V N A A K A G G L K K D S L L T V R  
 GCGTGGCGGCGCTGCGGCGAAGCGCGCGCTTGCGCTGCTGCGCGCGCTCAGCGAGCGACAGCA 120  
 L G A W G N P A P P S C G R L K E D S R  
 GGTACATCTTCTTCAATCGAGCGCGAGCGCGAAGCGAGCGCGCGCGCGCGCTGCGCGA 180  
 Y I F F H E P E A N S S G G P G R L P S  
 GCGTCTCTCGCGCGCTCTCGAGCGCGCGCGAAGCTCAGCGAGCGAGCTCAGCGCGCGCTGCTG 240  
 L L P P S R D G P E P Q E G G Q P G A V  
 TCGAAGCTGCG 252

FIGURE 31 (CONT.)

CODING SEGMENT B: (SEQ ID NO: 138)

L P P R L K E N K S Q E S V A G S K L V  
 CCTTGCCTCCCCGCTTGAAGAGATGAAGACTCAGGAGTCTGTGGCAGGTTCCAACTAG 60  
 |||||  
 ccttgcctccccgattgaaagagatgaaagccagggaatcggtgcagggtccaaactag  
 Q A  
  
 L R C E T S S E Y S S L K F K V P K N G  
 TCCTTCCTGCCAGACCACTTCTCAATACTCCTCTCTCAAGTTCAAGTCTTCAAGAAATC 120  
 |||||  
 tccttcggtgtgaaaccagtctctgaatactcctctctcagattcaagtgttcaagaatg  
 R  
  
 S E L S R K N K P Q N I K I Q K R P G  
 GGAGTGAATTAAGCCCAAGCAACCAACCAACATCAACATACAGCAAAAGCCCCCG 178  
 |||||  
 ggaatgaattgaatcgaaaaaaccaaccacaaaatatcaagatacaaaaaagccagg  
 M N X

CODING SEGMENT A: (SEQ ID NO: 139)

K S E L R I S K A S L A D S G E Y N C K  
 GAAGTCAGAACTTCCATTAGCAAGCCTCACTGGCTGATTCTGCAGAAATATATGTGCA 60  
 |||||  
 gaagtcaagacttcgcatttaacaaagcatcactgggtgattctggagagtatatgtgca  
 N  
  
 V I S K L G N D S A S A N I - I V E S N  
 AGTGATCAGCAAACTAGCAAAATCAAGTCCCTCTGCCAAACATCAACATTGTGAGTCAA 120  
 |||||  
 agtgatcagcaaaattaggaattgacgtgacctctgccaatatcaccaatctgggaatcaa  
 A  
 CG 122  
 ||  
 CG

CODING SEGMENT A': (SEQ ID NO: 140)

TCTAAAACCTACAGAGACTGTATTTCATGATCATCATAGTTCTGTCAAAATATACTTAAAC 60  
 K S E L R I S K A S L A D  
 CGCTTTGGTCTCTGATCTTGTAGCAAGTCAGAACTTCCGATTAGCAAGCCTCACTGGCTC 120  
 S G E Y N C K V I S K L G N D S A S A N  
 ATTCTGCAGAAATATATGTGCAAACTGATCAGCAAACTAGCAAAATCAAGTCCCTCTGCCA 180  
 I T I V E S N G K R C L L R A I S Q S I  
 ACATCACCAATTGTCCAGTCAAGCCTAAGAGATGCCCTACTGCCGTGCTATTCTCACTCTC 240  
 R G V K V C E N  
 TAAAGAGAGTCAATCAAGTATGTCTCTCACTTTCAATCAAGCAGGCTGTCTCAATCTCAT 300

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TGTCACAAATAAATCAATGAAAGGAAATCTCTATGTTTCAAAATATCTTATGGGTCTC 360  
 CTCTAAAGCTCTTCACTCCATAAGGTCAAATAGACCTGAAATATATATAGATTATTT 417

## CODING SEGMENT G: (SEQ ID NO: 141)

E I T T G N P A S T E T A Y V S S E S P I 60  
 AGATCACCACCTGGCATGCGAGCCTCACTGAGACAGCCTATCTGCTCTTCAGAGTCTCCCA  
 |||||  
 agatcatcactggtatgcccagcctcaactgaaggagcatatgtgtcttcagagtctccca  
 I

R I S V S T E G T N T S S S 102  
 TTAGAAATATCACTATCAACAGAAAGCAAAATACTTCTTCAAT  
 |||||  
 ttagaatatcagtatccacagaaaggagcaaatacttcttcat  
 A

## CODING SEGMENT G: (SEQ ID NO: 160)

T S T S T A G T S E L V K C A E K E K I 60  
 CCAATCCACATCTACAGCTGGGACAAAGCCATCTTGTCAAGTCTCCAGACAAAGCAAAA  
 |||||  
 ctacatctacatccaccactgggacaaagccatcttgtaaaaatgtgcggagaaaggagaaaa  
 T

F C V N G G E C F N V K D L S N P S R Y 120  
 CTTTCTCTGTCAATGCAAGCCCACTGCTTCAATGCTCAAAACCTTTCAAAATCCCTCAAGAT  
 |||||  
 ctttctgtgtgaatggaggggagtgcttcatgggtgaagacctttcaaaacctctcgagat

L C 128  
 ACTTCTCC  
 |||||  
 acttctgc

FIGURE 31 (CONT.)

CODING SEGMENT C/D: (SEQ ID NO: 142)

K C Q P G F T G A R C T E N V P N K V Q 60  
 AACTGCCAACCCTGGATTCACTGGAGCGAGATGTACTGAGAAATGTGCCCATGAAAGTCCAA  
 |||||  
 aagtgccaaacctggattcactggagcagagtggtactgagaatgtgcccatgaaagtccaa

T Q E  
 ACCCAAGAA 69  
 |||||  
 aaccaagaa  
 N

CODING SEGMENT C/D': (SEQ ID NO: 143)

K C P N E F T G D R C Q N Y V N A S F Y 60  
 AACTGCCAATAAGTTTACTGGTCAATGGCTGCCAATACTACGTAATGCCCAAGCTTCTAC  
 |||||  
 aagtgccaaatgagtttactggatgctgcccataactacgtaatggccagcttctac

CODING SEGMENT D: (SEQ ID NO: 144)

S T S T P F L S L P E 36  
 AGTACGTCCACTCCCTTTCTGTCTCTGCTTGAATAG  
 |||||  
 agtacgtccactccctttctgtctctgcttgaatag

CODING SEGMENT D': (SEQ ID NO: 145)

K E L G I E F N E  
 aagcatcttgggattgaatttatggag 27

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# SECRET

K A E E L Y Q K R V L T I T G I C I A L 60  
 A A C C C G A C C A G C T C T A C C A G A A G A G A C T G C T C A C C A T T A C C C C C A T T T G C A T C G C C C T G  
 A A G G C G G A G G A G C T G T A C C A G A A G A G A G T G C T G A C C A T A A C C G G C A T C T G C A T C G C C C T G  
 L V V G I N C V V V Y C K T K K Q R K K 120  
 C T C G T C C T T G C C A T C A T G T G T G T C C T G C T A C T G C A A A C C A A G A A A C A A C C C A A A A G  
 C T T G T G G T C G G C A T C A T G T G T G T G G T G G C T A C T G C A A A C C A A G A A A C A G C G G A A A A A G  
 L E D R L R Q S L R S E R N T N N N V A 180  
 C T T C A T G A C C C C C T T G C C A C A G C C T T C C C T G T G A A A C A A A C A C C A T C A T G A A C G T A G C C  
 C T G C A T G A C C C T C T T C G G C A G A G C C T T C G G T C T G A A C G A A A C A T A T G A T G A A C A T T G C C  
 K C P H E P N P P P E N V Q L V N Q Y V 240  
 A A C C G C C C C C A C C A C C C C A T C C G C C C C C C A G A A C G T G C A G C C T G C A A T C A A T A C G T A  
 A A T G G G C C T C A C C A T C C T A A C C C A C C C C C G A G A A T G T C C A G C T G G T G A A T C A A T A C G T A  
 S K N V I S S E N I V E R E A E S S P S 300  
 T C T A A A A T G T C A T C T C T A C C C A G C A T A T T G T T G A C A G A G A G C C C G A C A G C C T C T T T T T C C  
 T C T A A A A C G T C A T C T C C A G T G A G C A T A T T G T T G A G A G A G A A G C A G A G A C A T C C T T T T C C  
 T S H Y T S T A N H S T T V T Q T P S E 360  
 A C C A G T C A C T A C A C T T G C A C A C C T C A T C A T T C C A C T A C T G T C A C T C A G A C T C C C A G T C A C  
 A C C A G T C A C T A T A C T T C C A C A G C C C A T C A C T C C A C T A C T G T C A C C C A G A C T C C T A G C C A C  
 S W S N G H T E S I I S E S E S V I V N 420  
 A C C T G C A C C A T G C A C A C A C T G A A A C A T C A T T T C C C A A G C C A C T G T G T C A T C C T G A T C  
 A G C T G G A G C A A C G G A C A C A C T G A A A G C A T C C T T T C C G A A A G C C A C T C T G T A A T C G T G A T G  
 S S V E N S R E S S P T G G P R G R L N 480  
 T C A T C C C T A C A A A C A G T A C C C A C A C C A C C C C A C T G C C C C C C C C A C A G C C A C C T C T C A T  
 T C A T C C G T A G A A A C A G T A G G C A C A G C A G C C C A A C T G G G G G C C C A A G A G G A C G T C T T A A T  
 G L G G P R E C N S Y L R N A R E T P D 540  
 G C C T T G C C A G C C C C C T G T G A A T G T A A C A G C T T C C T C A C C C A T C C C A G A G A A A C C C C T G A C  
 G G C A C A G G A G G C C C T C G T G A A T G T A A C A G C T T C C T C A G G C A T G C C A G A G A A A C C C C T G A C  
 S Y R D S P H S E R 569  
 T C C T A C C G A G A C T C T C C T C A T A G T G A A A C  
 T C C C A C C G A G A C C C C C A T G T G A A A G

FIGURE 31 (CONT.)

CODING SEGMENT K: (SEQ ID NO: 161)

ACATAACCTTATAGCTGAGCTAAGGAGAAACAGGCCCAACAGATCCAAATGATCCAGAT  
 N N L I A E L R R N K A N R S K C N Q I  
 CCAAGCTTTCCGCAACTCATCTTACAGCTTCTTCCATTCCCCATTGGGCTTCATTCTCTAA  
 Q L S A T N L R A S S I P E N A S F S K  
 CACCCCTTGGCCTTLAGCAAG  
 T P N P L C R

CODING SEGMENT L: (SEQ ID NO: 147)

Y V S A N T T P A R N S P V D F N T P S  
 GTATGTATCAGCAATGACCAACCCCTCTCTATGTACCTGTAGATTTCACACCCCAAG 60  
 GTATGTGTGAGCCATGACCAACCCCTCTCTATGTACCTGTAGATTTCACACCCCAAG  
 S P K S P P S E N S P P V S S T T V S N  
 CTCCCCCAAGTCAACCCCTCTCTGAAATGTCTCCCGCCCTGTCCAGCAACCAAGCTCTCCAT 120  
 CTCCCCCAAGTCAACCCCTCTCTGAAATGTCTCCCGCCCTGTCCAGCAACCAAGCTCTCCAT  
 P S K A V S P P V E E E R P L L L V T P  
 GCGCTCCATGGCGCTCAGTCCCTCTCTGAAAGAGAGAGACCCCTGCTCTCTGTGACCCC 180  
 GCGCTCCATGGCGCTCAGTCCCTCTCTGAAAGAGAGAGACCCCTGCTCTCTGTGACCCC  
 P R L R E K Y D E N A Q Q P N S P E C  
 ACCACCGCTGCGGCAAG...TATCAACCAACCAACCAACCAATTCACCTCTCTCACTG 240  
 ACCACCGCTGCGGCAAG...TATCAACCAACCAACCAACCAATTCACCTCTCTCACTG  
 E P A N E S N S L P P S P L R I V E D E  
 CAAACCCCGCTCAGTCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCA 300  
 CAAACCCCGCTCAGTCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCA  
 E Y E T T Q E Y E P A Q E P V K K L T N  
 CGAATATGAAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCA 360  
 CGAATATGAAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCA  
 S S R R A K R T K P N G H I A N R L E N  
 CAGCAGCCCGCGCGGCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCA 420  
 CAGCAGCCCGCGCGGCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCA  
 ...TAGCCGCGCGGCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCA  
 N

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|   |     |
|---|-----|
| D N N T G A D S S N S S S T R D R V                             |     |
| CGACACACACACACCGCGCTGACAGCACTAACTCAGACAGCGGAAACAGAGGATGAAAGAGT  | 480 |
|   |     |
| ggacagcaacacaaagctcccagagcagtaactcagagagtgaaacagaaagatgaaagagt  |     |
| S S Q   |     |
| G E D T P P L A I Q N P L A A S L E A A                         |     |
| ACGAGAAGATACCCCTTCTCTGGCCATACAGAAACCCGCTGGCAGCCAGTCTCCAGCCGCC   | 540 |
|   |     |
| agggtgaagatacgcctttcctgggcatacagaacccccctggcagccagtccttgaggcacc |     |
| G   |     |
| P A F R L V D S R T N P T G G F S P Q E                         |     |
| CCCTGCGCTTCCGCGCTGCTGACAGCAGGACTAAACCCACACGCGCGCTTCTCTCCGCAGCA  | 600 |
|   |     |
| aactgccttccgcctgggtgacagcaggactaaccacagcaggccgcttctcagacacagga  |     |
| A A R   |     |
| E L Q A R L S G V I A N Q D P I A V                             |     |
| AGAAATTCACGCGCACGCTCTCCGCTGTAAATCGCTAACCAAGACCGTATCGCTGTCTAAA   | 660 |
|   |     |
| agaaatccaggccaggctgtctagtgttaattgctaaccgaagaccctattgctgtataaaa  |     |
| I S   |     |
| CGGAAATACACCCATAGATTCACTGTAAAACCTTATTTTATATAAATAAAGTATTCCACC    | 720 |
|   |     |
| cctaataaaacacatagattcacctgtaaaactttattttatataataaagtattccacc    |     |
| TTAAATTAAACA 733  |     |
|   |     |
| ttaaatttaaacaa  |     |

[illegible]



## GGP2BPP5 nucleotide sequence and deduced protein sequence

AGTTTCCCCCCCCAACTTGTCCAACTCTCCCTCCGCGCCAGGGCAGGAGCCGAGCCG 60  
 GCGCCCTGCTCCAGGCCATGCTAGCCGCGGCGCGGAGCCGTAATCCGCTCTCTCTCTCCG 120  
 TCCTAGCCCTCCCGGACCCAGCCAGCCAGCCAGCCGACCCGCGCGGAGCCGAGGACTCC 180  
 CCAAGCCGCGCTCCAGCCAGCCAGCCAGCCAGCCGAGCCGAGCCGAGCCGAGCCGAGCC 240  
 AGTCCCAAGCTGCGCGGAGCCAGCCAGCCAGCCAGCCAGCCGAGCCGAGCCAGCCAGCC 300  
 GCTCCCCCGGAGCCGCGCGGAGCCAGCCAGCCAGCCAGCCAGCCGAGCCAGCCAGCCAG 360  
 AACTTTTCTCCAGCCAGCCAGCCAGCCAGCCAGCCAGCCAGCCAGCCAGCCAGCCAGCC 420  
 CCGGAGCCGCTCCCGGAGCCAGCCAGCCAGCCAGCCAGCCAGCCAGCCAGCCAGCCAGCC 480  
 N S E R R E G  
 AAGCCAGCCGAGCCAGCCAGCCAGCCAGCCAGCCAGCCAGCCAGCCAGCCAGCCAGCC 540  
 K G K G K G G K K D R G S G K K P V P A  
 GCTCGCGCGCGGAGCCAGCCAGCCAGCCAGCCAGCCAGCCAGCCAGCCAGCCAGCCAGCC 600  
 A G C P S P A L P P R L K E H K S Q E S  
 CTCCAGCCGTTCCAACTAGCTCTCCCTCCAGCCAGCCAGCCAGCCAGCCAGCCAGCCAG 660  
 V A G S K L V L R C E T S S E Y S S L K  
 TTCAGCTCTCCAGCCAGCCAGCCAGCCAGCCAGCCAGCCAGCCAGCCAGCCAGCCAGCC 720  
 F K M P K M G S E L S R K N K P Q H I K  
 ATACAGCCAGCCAGCCAGCCAGCCAGCCAGCCAGCCAGCCAGCCAGCCAGCCAGCCAGCC 780  
 I Q K R P G K S E L R I S K A S L A D S  
 GAGCAATATATGTCAGCCAGCCAGCCAGCCAGCCAGCCAGCCAGCCAGCCAGCCAGCCAG 840  
 G E Y M C K V I S K L G H D S A S A N I  
 ACCATTCTGAGCTCCAGCCAGCCAGCCAGCCAGCCAGCCAGCCAGCCAGCCAGCCAGCCAG 900  
 T I V E S H E I T T G M P A S T E T A Y  
 GTGTCTTCCAGCTCTCCAGCCAGCCAGCCAGCCAGCCAGCCAGCCAGCCAGCCAGCCAGCC 960  
 V S S E S P I R I S V S T E G T H T S S  
 TCCAGCTCCAGCTCTCCAGCCAGCCAGCCAGCCAGCCAGCCAGCCAGCCAGCCAGCCAGCC 1020  
 S T S T S T A G T S H L V K C A E K E K  
 ACTTTCTGTCTGAAATGAGCCAGCCAGCCAGCCAGCCAGCCAGCCAGCCAGCCAGCCAGCC 1080  
 T P C V M G G E C P M V K D L S H P S R  
 TACTTCTCCAGCTCCAGCCAGCCAGCCAGCCAGCCAGCCAGCCAGCCAGCCAGCCAGCCAG 1140  
 Y L C K C P M E P T G D R C Q H Y V M A  
 AGCTTCTACAGTACCTCCAGCTCCAGCTCCAGCTCCAGCTCCAGCTCCAGCTCCAGCTCC 1200  
 S F Y S T S T P F L S L P E  
 GTCCCGCTTTCT 1260  
 CT

FIGURE 32 (CONT.)

TGA CTTCCTCTCTCCGTCACTAGTGGGCTCTGAGCTACTCGTAGCCTAAGGCTCCAG 1380  
 TGT TTTCTCAATTCAATCTTCAATTACTGTCTATAGGACATCATAGTCCCTCTCA CCGAGTG 1440  
 CAATGACCAATAAAGCCCTTCAAAAAGTCTCACTTTTATTGAGAAAATAAAAATCGTTCCAG 1500  
 GCGACAGTCCCTCTTCTTTATAAAAATGACCTATCTTGA AAAAGGAGGTCTGTAAAGTTG 1560  
 TAA CCACTACACACTTCAAAATCATCTAAAGTTCCGCTTCCGTTCA GAATCTCTTCTTTCTG 1620  
 ACA AATAAACAGAAATAAAAAA 1653

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## GGP2BPP2 nucleotide sequence and deduced protein sequence

CATCATGTGTGGGCGGCGAAGCGGCGGCGGCTTCAAGAACTCGCTGCTCAAGCTGCGG 60  
 H Q V W A A K A G G L K K D S L L T V R  
 CTGCGGCGGCTGCGGCGGCGGCGGCGGCTTCCGCTGCTGCGGCGGCGGCTCAAGCGGCGGCGG 120  
 L G A N G H P A P P S C G R L K S D S R  
 TACATGTTTCTTCATGCAAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 180  
 Y I P P H E P E A N S S G G P G R L P S  
 CTGCTTCCGCGGCTGCTCAAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 240  
 L L P P S R D G P E P Q E G G P G A V  
 CAACTGTGCGGCGGCTTCCGCTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 300  
 Q R C A L P P R L I E H K S Q E S V A G  
 TCCAACTAGTGTGCTTCCGCTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 360  
 S K L V L R C E T S S E Y S S L K P K N  
 CTCAACTAGTGTGCTTCCGCTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 420  
 P K N G S E L S R I H K P E H I E I Q K  
 AGCGCGG 480  
 R P G K S E L R I S K A S L A D S G E Y  
 ATGTCCAACTAGTGTGCTTCCGCTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 540  
 K C K V I S K L G H D S A S A H I T I V  
 GAGTCCAACTAGTGTGCTTCCGCTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 600  
 E S N A T S T S T A G T S E L V K C A E  
 AAGGCGG 660  
 K E K T P C V H G G E C P H V K D L S H  
 CCTTCAAGCTAGTGTGCTTCCGCTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 720  
 P S R Y L C K C Q P G P T G A R C T E H  
 GTGCGG 780  
 V P H K V Q T Q E E C P H E P T G D R C  
 CAACTAGTGTGCTTCCGCTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 840  
 Q H Y V H A S P Y S T S T P P L S L P E  
 TAGCGCATCTCACTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 900  
 \*  
 AGCTAGATGCGGTTTTACCAAGGTCTAACATGACTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 960  
 AACACAAAGCGATTGTATGACTTCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1020  
 GTCCCTAAGGCTCCAGTGTCTTCTCAATTCTATCTCAATTACTGCTATCTGACATCATAG 1080  
 TCCCTCTCAAGGCTCCAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1140

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## GGF2BPP4 nucleotide sequence and deduced protein sequence

GAAGTCAGAACTTCCGATTAGCAAGCGTCACTGGCTGATTCTCGAGAAATATGTGCCAA 60  
 K S E L R I S K A S L A D S G E Y M C K  
 AGTCATCAGCAAACTAGCAATGACAGTGCCTCTGCCAAATCACCATTGTGGAGTCAAA 120  
 V I S K L G N D S A S A N I T I V E S N  
 CGCCACATCCACATCTACAGCTGGCAAAAGCCATCTTGTCAAGTGTGCAGAGAGGAGAA 180  
 A T S T S T A G T S E L V K C A E K E K  
 AACTTTCTGTGTGAATGGAGCGGACTGCTTCATGGTGAAAGACCTTTCAATCCCTCAAG 240  
 T F C V N G G D C F M V K D L S N P S R  
 ATACTTCTGCAAGTCCCAAGCTGGAATTCACTGGAGCCAGATGTACTGCAATGTGCCCCAT 300  
 Y L C K C Q P G F T G A R C T E N V P M  
 GAAAGTCCAAACCCAGAAAGAGCGGAGGAGCTGTACCAAGAGAGAGTGCCTCACCATTAC 360  
 K V Q T Q E K A E E L Y Q K R V L T I T  
 CGGCATTTGCAATCGCGCTGCTGCTGCTTGGCATCATGTGTGTGCTGCTTACTGCCAAAC 420  
 G I C I A L L V V G I N C V V V Y C K T  
 CAAGAAACAAACGAAAGAGCTTCATGACCGGCTTCCGCAAGGCTTCCGCTGTCAAAAGAA 480  
 K K Q R K K L E D R L R Q S L R S E R N  
 CACCATGATCAACCTAGCCAAAGGCGCCCAACCAACCCCAATCCGCCCCCGAGAACCTGCCA 540  
 T H N N V A N G P H E P N P P P E N V Q  
 CCTCGTGAATCAATACGTATCTAAAAATGTTCATCTCTAGCCAGCATATTGTTCAGAGAGA 600  
 L V N Q Y V S K N V I S S E H I V E R E  
 GCGGAGAGCTCTTTTTCACCAAGTCACTACACTTCCACAGCTCATCATTTCCACTACTGT 660  
 A E S S F S T S E Y T S T A E E S T T V  
 CACTCAGACTCCCACTCAAGCTCCAGCAATGGACACACTGAAAGCATATTTCGGAAG 720  
 T Q T P S E S M S N G H T E S I I S E S  
 CCACTCTGTCACTGCTCATGTTCCTTAGCAAAACAGTAGCCACAGCAGCCCCCACTGGGGG 780  
 H S V I V N S S V E N S R E S S P T G G  
 CCCCCAGGAGCTCTCAATGGCTTGGAGCGGCTCTGTCAATGTAAACAGCTTCTCAGCCCA 840  
 P R G R L N G L G G P R E C H S P L R E  
 TGCCACAGCAAAACCCCTCACTGCTACCGAGACTCTGCTCATAGTCAAAACATAACCTTAT 900  
 A R E T P D S Y R D S P H S E R E N L I  
 AGCTGAGCTAAGGAGAAACAAAGGCCACAGATCCAAATGCAAGCAGATCCAGCTTTCCGG 960  
 A E L R R N K A E R S K C M Q I Q L S A  
 AACTCATCTTAGAGCTTCTTCCATTCCCCATTGGGCTTCAATTCTTAAGACCCCTTGGCC 1020  
 T H L R A S S I P H W A S F S K T P W P  
 TTLAGCAAGCTATCTATCAGCAATGACCACCCCGGCTCTATGTACCTGTAGATTTCCA 1080  
 L C R Y V S A M T T P A R M S P V D F H  
 CACCCCAAGCTTCCCAAGTCAACCCCTTCCCAATGTCTCTCCCTGTCTCAGCAGCAAC 1140  
 T F E S F K S F P S E M S P P V S S T T

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FIGURE 34 (CONT.)

GGTCTCCATGCCCTCCATGCGCGTCACTCCCTTCTGGAAGAGGAGAGACCCCTGCTCTT 1200  
 V S N P S N A V S P P V E E E R P L L L  
 TGTACGCCACCACTGCGCGGAGAGTATGACCAACCAAGCCCAAGCAATTCACTCTT 1260  
 V T P P R L R E K Y D H H A Q Q P N S F  
 CCACTGCAACCCCGCGCATGAGAGCAACAGCCTGCCCCCAGCCCCCTGAGGATAGTGA 1320  
 H C N P A H E S N S L P P S P L R I V E  
 GCAATGAGCAATATGAAACGACCCAGAGTACCAACCAAGCTCAAGAGCCCGTTAAGAACT 1380  
 D E E Y E T T Q E Y E P A Q E P V K K L  
 CACCAACAGCAGCCCGCGCGCCAAAGCAACCAAGCCCAATGCTCAATTGCCCAAGCTT 1440  
 T N S S R R A K R T K P N G H I A E R L  
 GCAATGCAACCAACCAACAGCCCGTACAGCAGTAACTCAGAGAGCCAAACAGAGGATCA 1500  
 E N D N N T G A D S S N S E S E T E D E  
 AAGACTAGGAGCAAGATACGCGCTTCTGCGCATACAGAAACCCCTGCGAGCCAGTCTCA 1560  
 R V G E D T P P L A I Q N P L A A S L E  
 GCGCGCGCGCTGCGCTTCCCGCTGCTCAACAGGAGTAAACCAACAGCGCGCTTCTCTCC 1620  
 A A P A P R L V D S R T N P T G G P S P  
 CCAGCAAGCAATTGCAAGCCAGCGCTCTCGGTATAATCGCTAACCAAGACCCCTATCGCTGT 1680  
 Q E E L Q A R L S G V I A N Q D P I A V  
 CTAAACCGAAATACACCCATAGATTCACTGTAAAACTTTATTTTATATATAAAGTAT 1740  
 TCCACCTTAATTAAACAAAA 1764

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FIGURE 35

GGF2~~MS~~KCAEKEKTFQVNGGECFMYKDLSNPSRYLCKCPNEFTGDRQNYVMASFY<sup>1</sup>  
GGF2~~MS~~KCAEKEKTFQVNGGDCFMYKDLSNPSRYLCKCQPGFTGARCTENVPMKVQ<sup>2</sup>  
HEGE ECLRKYKDFCIH - GECKYKELRAPS — CKCQOQETFGERCGEKSNKTHS<sup>3</sup>

<sup>1</sup>(SEQ ID NO: 151)

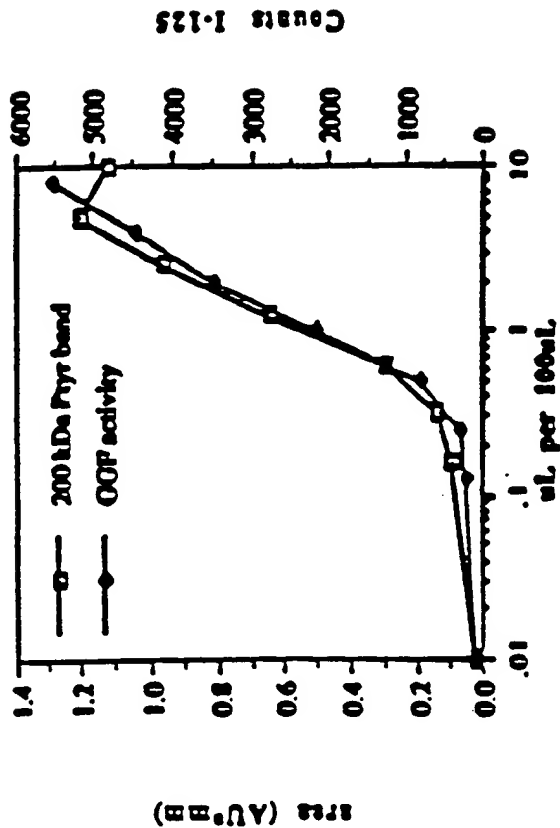
<sup>2</sup>(SEQ ID NO: 152)

<sup>3</sup>(SEQ ID NO: 153)

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FIGURE 36

# 200 kDa tyrosine phosphorylation compared with mitogenic activity



## GGT/HERPESVIRUS SPLICING VARIANTS

Y-B-A'

Y-B-A-C-C/D-D  
 Y-B-A-C-C/D-H  
 Y-B-A-C-C/D-H-L  
 Y-B-A-C-C/D-H-K-L  
 Y-B-A-C-C/D-D'-H  
 Y-B-A-C-C/D-D'-H-L  
 Y-B-A-C-C/D-D'-H-K-L  
 Y-B-A-C-C/D'-D  
 Y-B-A-C-C/D'-H  
 Y-B-A-C-C/D'-H-L  
 Y-B-A-C-C/D'-H-K-L  
 Y-B-A-C-C/D'-D'-H  
 Y-B-A-C-C/D'-D'-H-L  
 Y-B-A-C-C/D'-D'-H-K-L  
 Y-B-A-C-C/D-C/D'-D  
 Y-B-A-C-C/D-C/D'-H  
 Y-B-A-C-C/D-C/D'-H-L  
 Y-B-A-C-C/D-C/D'-H-K-L  
 Y-B-A-C-C/D-C/D'-D'-H  
 Y-B-A-C-C/D-C/D'-D'-H-L  
 Y-B-A-C-C/D-C/D'-D'-H-K-L

Y-B-A-G-C-C/D-D  
 Y-B-A-G-C-C/D-H  
 Y-B-A-G-C-C/D-H-L  
 Y-B-A-G-C-C/D-H-K-L  
 Y-B-A-G-C-C/D-D'-H  
 Y-B-A-G-C-C/D-D'-H-L  
 Y-B-A-G-C-C/D-D'-H-K-L  
 Y-B-A-G-C-C/D'-D  
 Y-B-A-G-C-C/D'-H  
 Y-B-A-G-C-C/D'-H-L  
 Y-B-A-G-C-C/D'-H-K-L  
 Y-B-A-G-C-C/D'-D'-H  
 Y-B-A-G-C-C/D'-D'-H-L  
 Y-B-A-G-C-C/D'-D'-H-K-L  
 Y-B-A-G-C-C/D-C/D'-D  
 Y-B-A-G-C-C/D-C/D'-H  
 Y-B-A-G-C-C/D-C/D'-H-L  
 Y-B-A-G-C-C/D-C/D'-H-K-L  
 Y-B-A-G-C-C/D-C/D'-D'-H  
 Y-B-A-G-C-C/D-C/D'-D'-H-L  
 Y-B-A-G-C-C/D-C/D'-D'-H-K-L

Y-Z-B-A'

Y-Z-B-A-C-C/D-D  
 Y-Z-B-A-C-C/D-H  
 Y-Z-B-A-C-C/D-H-L  
 Y-Z-B-A-C-C/D-H-K-L  
 Y-Z-B-A-C-C/D-D'-H  
 Y-Z-B-A-C-C/D-D'-H-L  
 Y-Z-B-A-C-C/D-D'-H-K-L  
 Y-Z-B-A-C-C/D'-D  
 Y-Z-B-A-C-C/D'-H  
 Y-Z-B-A-C-C/D'-H-L  
 Y-Z-B-A-C-C/D'-H-K-L  
 Y-Z-B-A-C-C/D'-D'-H  
 Y-Z-B-A-C-C/D'-D'-H-L  
 Y-Z-B-A-C-C/D'-D'-H-K-L  
 Y-Z-B-A-C-C/D-C/D'-D  
 Y-Z-B-A-C-C/D-C/D'-H  
 Y-Z-B-A-C-C/D-C/D'-H-L  
 Y-Z-B-A-C-C/D-C/D'-H-K-L  
 Y-Z-B-A-C-C/D-C/D'-D'-H  
 Y-Z-B-A-C-C/D-C/D'-D'-H-L  
 Y-Z-B-A-C-C/D-C/D'-D'-H-K-L

Y-Z-B-A-G-C-C/D-D  
 Y-Z-B-A-G-C-C/D-H  
 Y-Z-B-A-G-C-C/D-H-L  
 Y-Z-B-A-G-C-C/D-H-K-L  
 Y-Z-B-A-G-C-C/D-D'-H  
 Y-Z-B-A-G-C-C/D-D'-H-L  
 Y-Z-B-A-G-C-C/D-D'-H-K-L  
 Y-Z-B-A-G-C-C/D'-D  
 Y-Z-B-A-G-C-C/D'-H  
 Y-Z-B-A-G-C-C/D'-H-L  
 Y-Z-B-A-G-C-C/D'-H-K-L  
 Y-Z-B-A-G-C-C/D'-D'-H  
 Y-Z-B-A-G-C-C/D'-D'-H-L  
 Y-Z-B-A-G-C-C/D'-D'-H-K-L  
 Y-Z-B-A-G-C-C/D-C/D'-D  
 Y-Z-B-A-G-C-C/D-C/D'-H  
 Y-Z-B-A-G-C-C/D-C/D'-H-L  
 Y-Z-B-A-G-C-C/D-C/D'-H-K-L  
 Y-Z-B-A-G-C-C/D-C/D'-D'-H  
 Y-Z-B-A-G-C-C/D-C/D'-D'-H-L  
 Y-Z-B-A-G-C-C/D-C/D'-D'-H-K-L

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## GGT/HIDROLIN SPLICING VARIANTS CONTINUED

E-B-A'

E-B-A-C-C/D-D  
 E-B-A-C-C/D-H  
 E-B-A-C-C/D-H-L  
 E-B-A-C-C/D-H-X-L  
 E-B-A-C-C/D-D'-H  
 E-B-A-C-C/D-D'-H-L  
 E-B-A-C-C/D-D'-H-X-L  
 E-B-A-C-C/D'-D  
 E-B-A-C-C/D'-H  
 E-B-A-C-C/D'-H-L  
 E-B-A-C-C/D'-H-X-L  
 E-B-A-C-C/D'-D'-H  
 E-B-A-C-C/D'-D'-H-L  
 E-B-A-C-C/D'-D'-H-X-L  
 E-B-A-C-C/D-C/D'-D  
 E-B-A-C-C/D-C/D'-H  
 E-B-A-C-C/D-C/D'-H-L  
 E-B-A-C-C/D-C/D'-H-X-L  
 E-B-A-C-C/D-C/D'-D'-H  
 E-B-A-C-C/D-C/D'-D'-H-L  
 E-B-A-C-C/D-C/D'-D'-H-X-L

E-B-A-G-C-C/D-D  
 E-B-A-G-C-C/D-H  
 E-B-A-G-C-C/D-H-L  
 E-B-A-G-C-C/D-H-X-L  
 E-B-A-G-C-C/D-D'-H  
 E-B-A-G-C-C/D-D'-H-L  
 E-B-A-G-C-C/D-D'-H-X-L  
 E-B-A-G-C-C/D'-D  
 E-B-A-G-C-C/D'-H  
 E-B-A-G-C-C/D'-H-L  
 E-B-A-G-C-C/D'-H-X-L  
 E-B-A-G-C-C/D'-D'-H  
 E-B-A-G-C-C/D'-D'-H-L  
 E-B-A-G-C-C/D'-D'-H-X-L  
 E-B-A-G-C-C/D-C/D'-D  
 E-B-A-G-C-C/D-C/D'-H  
 E-B-A-G-C-C/D-C/D'-H-L  
 E-B-A-G-C-C/D-C/D'-H-X-L  
 E-B-A-G-C-C/D-C/D'-D'-H  
 E-B-A-G-C-C/D-C/D'-D'-H-L  
 E-B-A-G-C-C/D-C/D'-D'-H-X-L

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EGFL1

AGCCATCTTGTCAAGTGTGCAGAGAGGAGAAAACTTTCTGTGTCAATGGAGGGGAGTGC  
S H L V K C A E K E K T P C V N G G E C  
TTCATGCTGAAAGACCTTTCAAATCCCTCAAGATACTTGTGCAAGTGGCCAAATGAGTTT  
P H V K D L S N P S R Y L C K C P N E P  
ACTGCTGATCGCTGCCAAACTACGTAATGGCCAGCTTCTACAGTACGTCCACTCCCTTT  
T G D R C Q N Y V H A S P Y S T S T P P  
CTGTCTCTGCCTGAATAG  
L S L P E \*

(SEQ ID NO: 154)

FIGURE 38

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ECFL2

AGCCATCTTGTCAAGTGTGCAAGAGAAGGAGAAAACTTTCTGTGTGAATGGAGCCGAGTGC  
S H L V K C A E K E K T F C V N G G E C  
TTCATGCTGAAAGACCTTTCAAATCCCTCAAGATACTTGTGCAAGTCCCAACCTGGATTG  
F H V K D L S H P S R Y L C K C Q P Q P  
ACTGGAGCCGAGATGTAAGTGAAGATGTGCCCATGAAAGTCCAAACCCCAAGAAAAAGCCGAG  
T G A R C T E N V P H K V Q T Q E K A E  
GAGCTCTACTAA  
E L Y \*

(SEQ ID NO: 155)

FIGURE 39

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207L3

AGCCATCTTGTCAAGTGTGCAGAGAGGAGAAAACTTTCTGTGTGAATGCAGGCCGACTGC  
S H L V K C A E K E K T F C V N G G E C  
TTCATGCTGAAAGACCTTTCAAATCCCTCAAGATACTTGTGCAAGTGCCCAAATGAGTTT  
F H V K D L S N P S R Y L C K C P N E F  
ACTGCTGATCCCTGCCAAACTACCTAATGCCAGCTTCTACAAAGCCGAGGAGCTCTAC  
T G D R C Q N Y V H A S F Y K A E E L Y  
TAA  
.

(SEQ ID NO: 156)

FIGURE 40

08736019-102296  
95220T-6T09E780



EGFLA

AGCCATCTTGTCAAGTGTGCAGAGAACGAGAAAACCTTTCTGTCTCAATCGAGGGCAGTGC  
S H L V K C A E K E K T P C V N G G E C  
TTCATGCTGAAAGACCTTTCAATCCCTCAAGATACTTGTCAAGTCCCCTCAATGAGTTT  
P N V K D L S N P S R Y L C K C P N E P  
ACTGCTGATCCCTGCCAAACTAGGTAATGCCAGCTTCTACCAAGCATCTTGGGATTGAA  
T G D R C Q N Y V N A S P Y K H L G I E  
TTTATGGAGAAAGCGGAGGAGCTCTACTAA  
P N E K A E E L Y •

(SEQ ID NO: 157)

FIGURE 41

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EGFLS

AGCCATCTTGTCAAAGTGTGCAGAGAACGAGAAAACTTTCTGTGTGAATGGAGGCGAGTGC  
S H L V K C A E K E K T F C V N G G E C  
TTCATGCTGAAAGACCTTTCAATCCCTCAAGATACTTGTGCAAGTGGCAACCTGGATTG  
F H V K D L S N P S R Y L C K C Q P G F  
ACTGGAGCGAGATGTACTGAGAATGTGCCCATGAAAGTCCAAACCCAGAAAAGTCCCA  
T G A R C T E N V P H K V Q T Q E K C P  
AATGAGTTTACTGGTGATCGCTGCCAAAACCTACGTAATGCCAGCTTGTACAGTACGTCC  
N E F T G D R C Q N Y V H A S P Y S T S  
ACTCCCTTTCTGTCTGTGCTGCTGAATAG  
T P F L S L P E \*

(SEQ ID NO: 158)

FIGURE 42

08736019-102296

20716

AGCCATCTTCTCAAGTGTGCAGAGAACGAGAAAACTTTCTGTGTGAATGGAGGCGAGTGC  
S H L V K C A E K E K T P C V H G G E C  
TTGATCGGTGAAAGACCTTTCAATCCCTCAAGATACTTGTGCAAGTCCCAACCTCGATTG  
P H V K D L S H P S R Y L C K C Q P G F  
ACTCGACCGAGATGTACTGAGAAATGTGCCCATGAAAGTCCAAACCCAAAGAAAAGTCCCA  
T G A R C T E H V P H K V Q T Q E K C P  
AATGAGTTTACTCGGTGATCGGTGCCAAACTACGTAATGCCAGCTTCTACAAAGCGGAG  
H E F T G D R C Q H Y V H A S F Y K A E  
GAGCTCTACTAA  
E L Y \*

(SEQ ID NO: 159)

FIGURE 43

03736019-1032296

**SECRET**

## GGF2HBS5

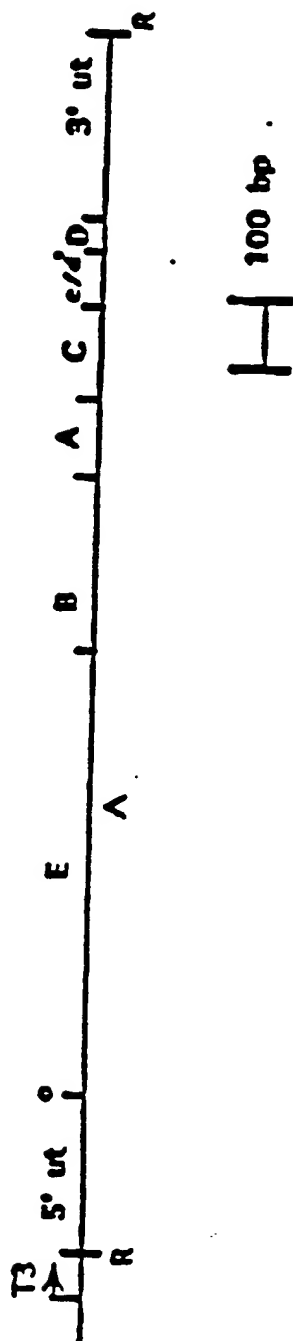


FIGURE 44

**SECRET**

(SEQ ID NO: 167)

FIGURE 45 (1 of 3)

03736019-102296

780  
E P G E E A P Y L V K V E Q V W A V E A  
K V E Q V W A A E  
GCTII-1 & GCTII-11

840  
G G L E X D S L L T V R L O T W G I P A  
D L L L I V L G A W G P P A  
GCTII-10 1 GCTII-3

900  
P P S C G R L E D S R Y I P P M E P D  
P P V X Y Y I P P M E P E  
GCTII-2

960  
A M S T S R A P A A P R A S P P P L E T  
A X S S G

1020  
G R M L E X E V S R V L C E R C A L P P

1080  
G L E X E M X S Q E S A A G S E L V L R C  
L V L R  
GCTII-6

1140  
E T S S E Y S S L R P X M P E N G E L

1200  
M E X M X P G N I X I Q E X P O E S E L

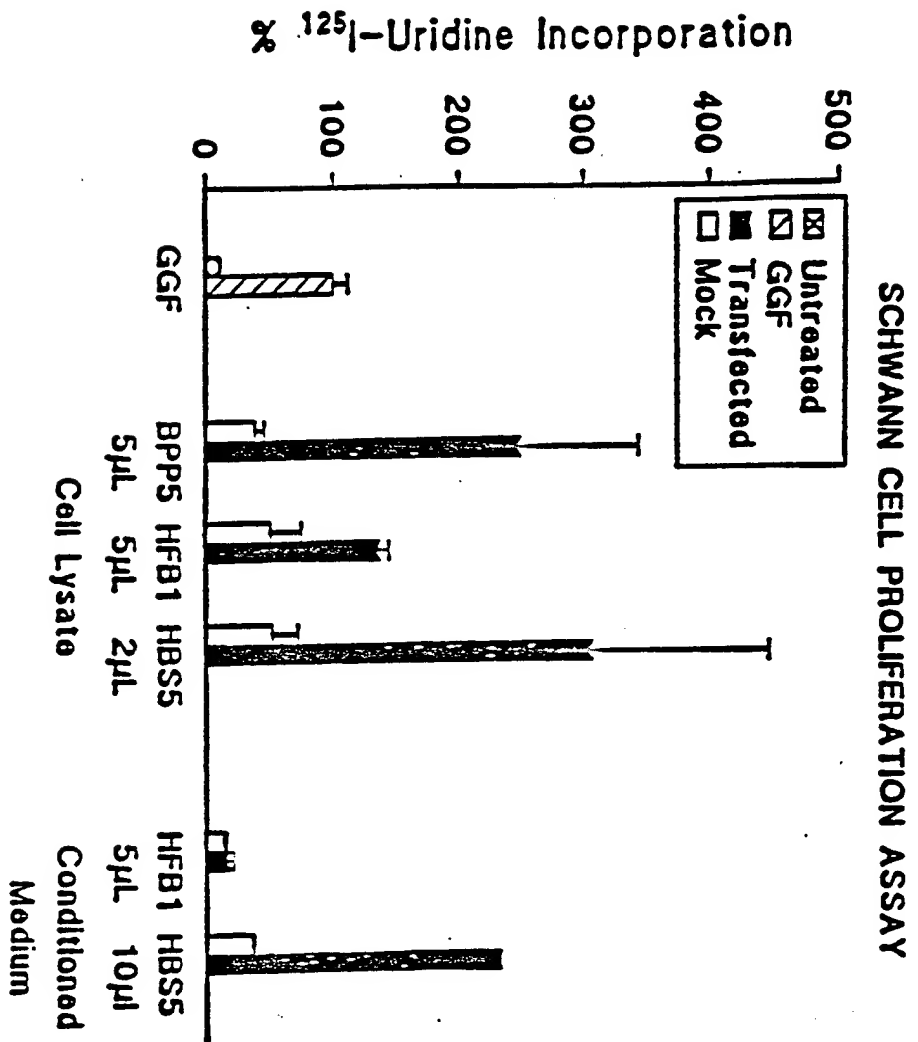
1260  
E I N E A S L A D S G E Y M C E V I S X  
K A S L A D S G E Y M X X  
GCTII-12

1320  
L O N D S A S A N I T I V E S N A T S T

FIGURE 45 (2 of 3)



FIGURE 46



08736019.102296



FIGURE 47

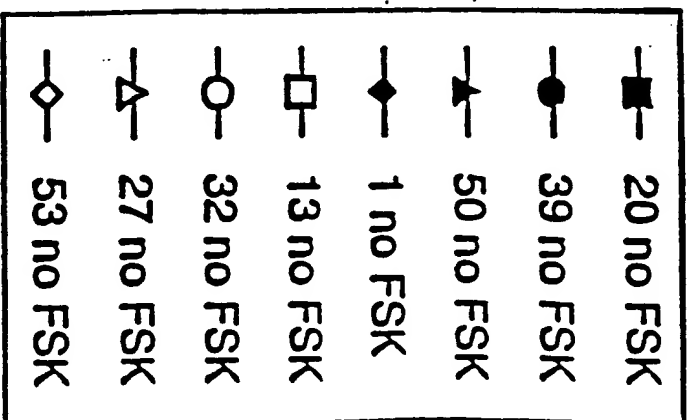
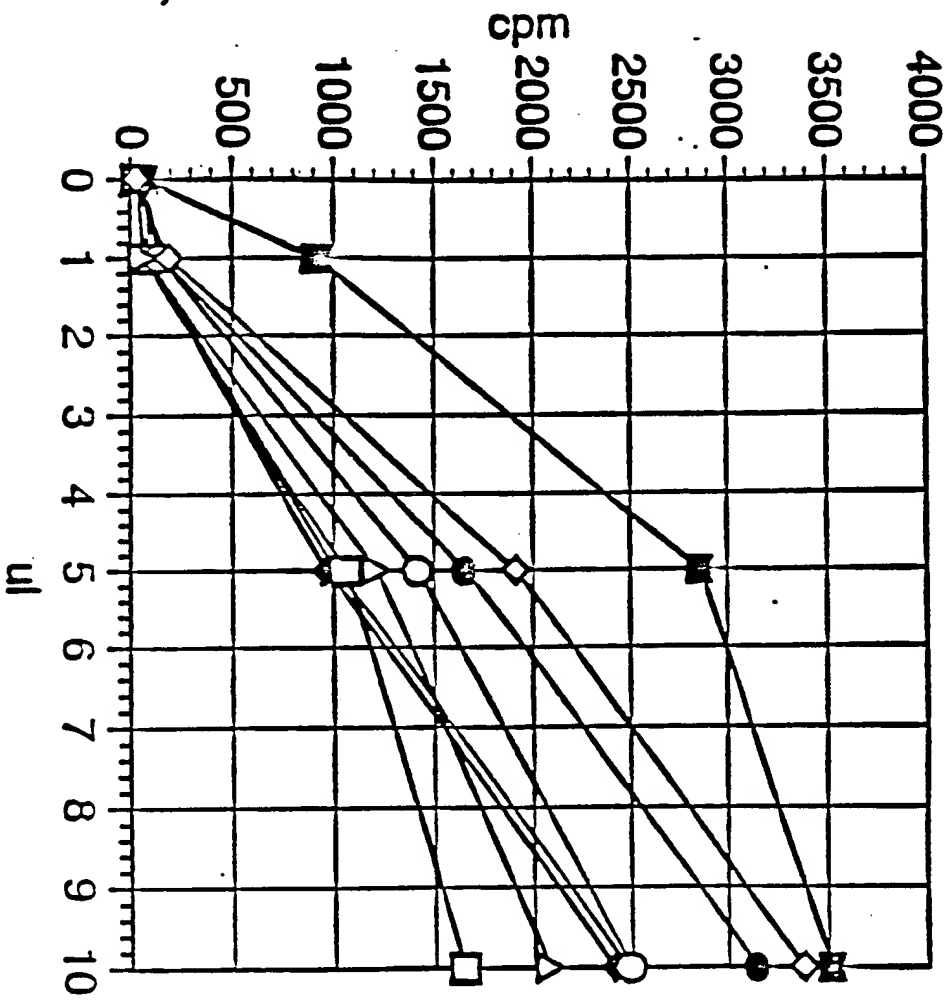


FIGURE 48

Schwann Cell Assay/Baculovirus Clones

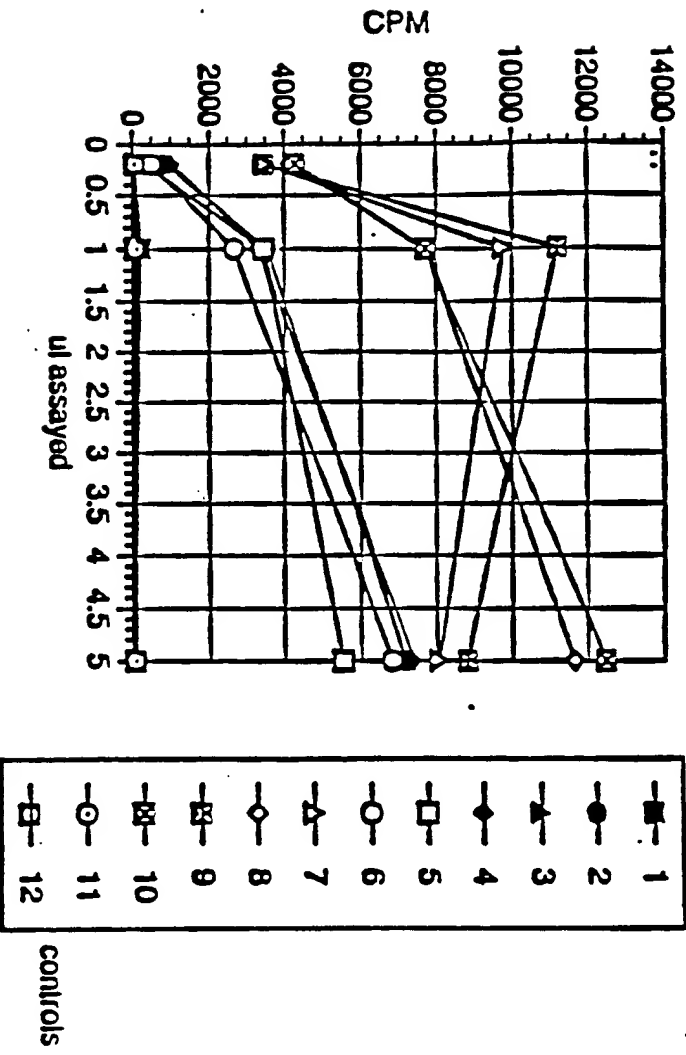
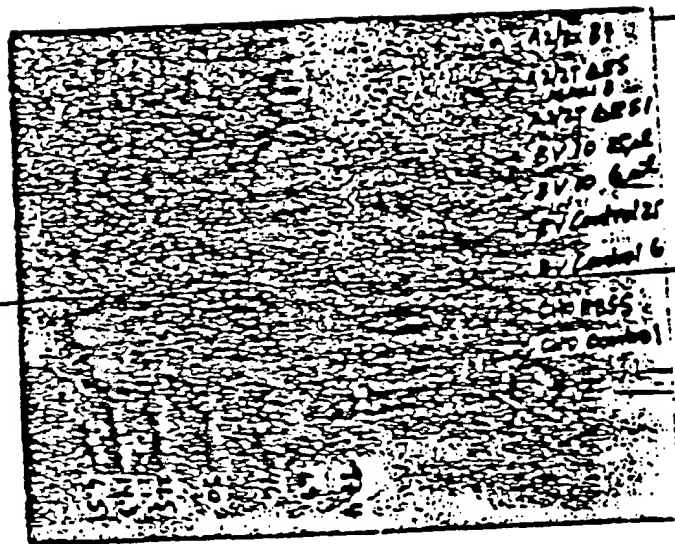
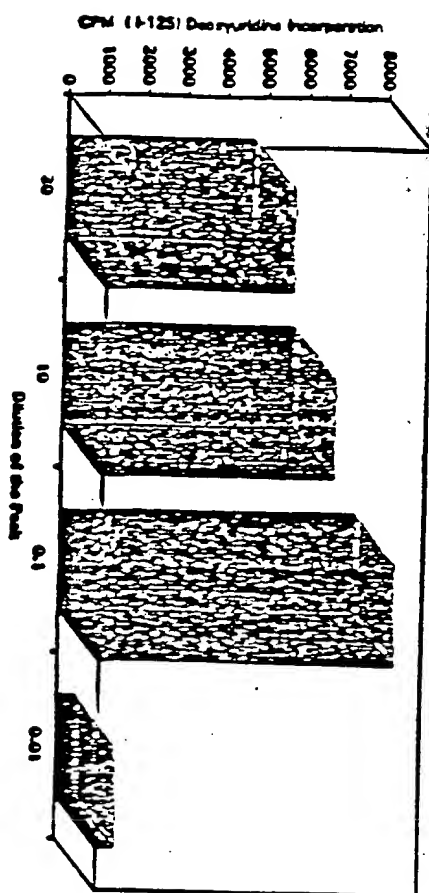


FIGURE 49



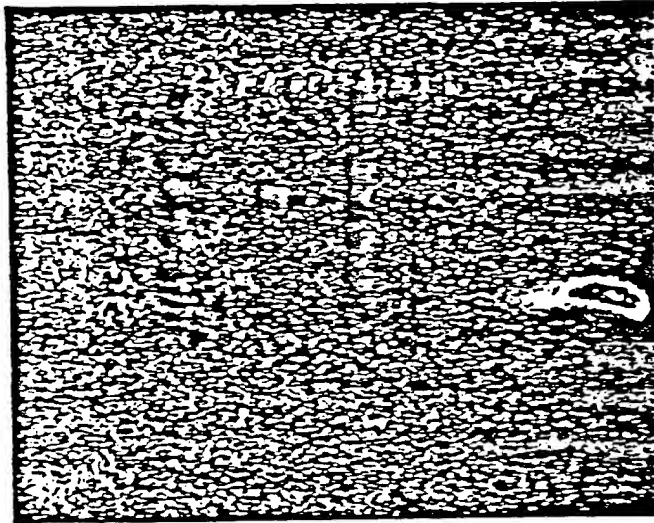
08736019.102996

FIGURE 50A



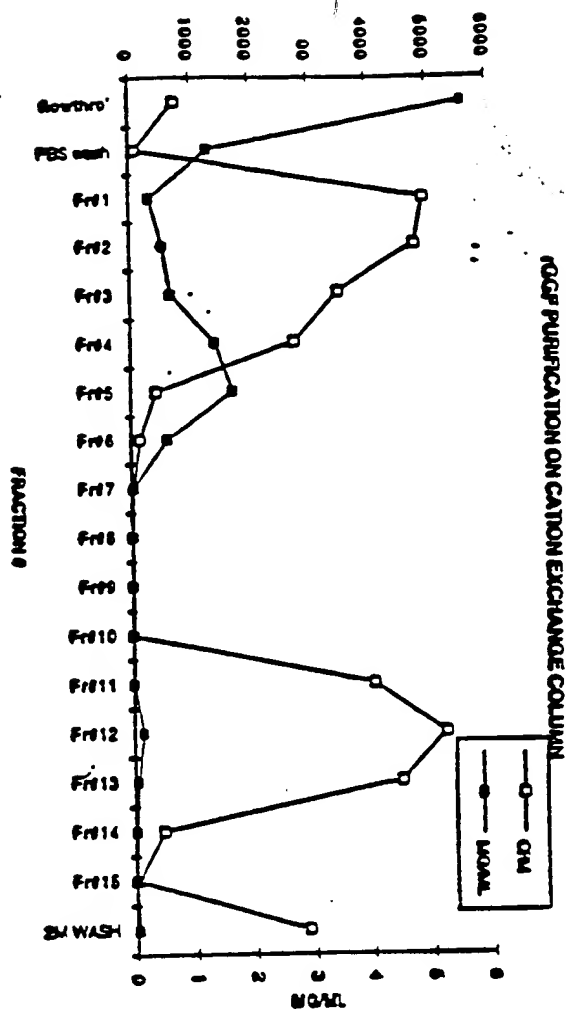
08736019.102296

FIGURE 50B



08736019-102296

**FIGURE 51**



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FIGURE 52 .

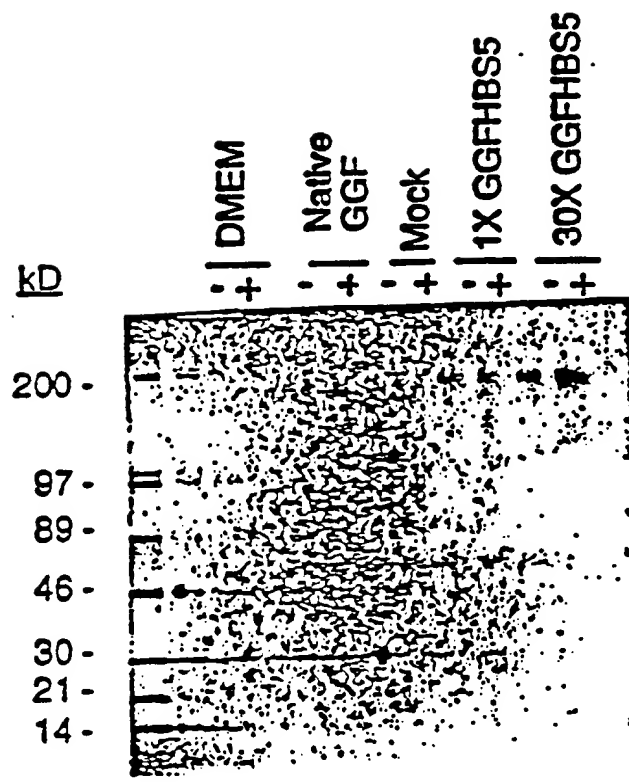






FIG. 5A

